

Rooke  
10/822-254 Page 1  
Seq. ID 6 w/ Interf

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	Result No.	Score	Query	Match	Length	DB	ID	Description
OM protein - protein search, using sw model	1	554	100.0	109	34	US-10-822-254-6		Sequence 6, Appli
Run on: February 16, 2005, 08:21:09 ; Search time 496 Seconds (without alignments)	2	551	99.5	109	34	US-10-822-254-6		Sequence 10, Appli
256.679 Million cell updates/sec	3	548	98.9	109	34	US-10-822-254-6		Sequence 88970, A
Title: US-10-822-254-6	4	548	98.9	109	34	US-10-822-254-6		Sequence 2, Appli
Perfect score: 554	5	548	98.9	138	21	US-09-724-676-50031		Sequence 50031, A
Sequence: 1 SQIPASQETLVPRPKPLK. .... .NLVVNQESSSDSGTYSSEN 109	6	548	98.9	138	21	US-09-724-676-50032		Sequence 50032, A
Scoring table: BL0SM62	7	548	98.9	138	21	US-09-724-676A-50031		Sequence 50031, A
Gapop 10.0 , Gapext 0.5	8	548	98.9	138	21	US-09-724-676A-50032		Sequence 50032, A
Searched: 6959266 seqs, 1168005243 residues	9	548	98.9	209	21	US-09-724-676A-50030		Sequence 50030, A
Total number of hits satisfying chosen parameters: 6959266	10	548	98.9	209	21	US-09-724-676A-50030		Sequence 50030, A
Minimum DB seq length: 0	11	548	98.9	253	35	US-10-990-328-10898		Sequence 10898, A
Maximum DB seq length: 2000000000	12	548	98.9	253	37	US-61-505-218-571		Sequence 571, Appli
Post-processing: Minimum Match 0%	13	548	98.9	491	1	PCT-US01-19888-1		Sequence 1, Appli
Maximum Match 100%	14	548	98.9	491	1	PCT-US02-29780-8		Sequence 8, Appli
Listing First 45 summaries	15	548	98.9	491	1	PCT-US03-34636-22		Sequence 22, Appli
Database :	16	548	98.9	491	1	PCT-US03-38193-2236		Sequence 2236, Appli
Pending Patents AA_Main.*	17	548	98.9	491	1	PCT-US04-12347-1		Sequence 1, Appli
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/cgn2_6/_picodata/1/paa/US24_COMB.pep:*	37	548	98.9	491	30	US-10-422-807-28		Sequence 8, Appli
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT 1  
US-10-822-254-6

GENERAL INFORMATION:

SEQUENCE 6, Application US/10822254

APPLICANT: Tareni, S. S.

Xie, Gaoian

Hesson, Thomas E.

Ducas, Jose S.

Strickland, Corey

Windor, William

Madsion, Vincent

Zhang, Rumin

Reichert, Paul

TITLE OF INVENTION: Soluble, Stable Form of Hdm2, Crystalline Forms Thereof and Methods

FILE REFERENCE: JBO6017031

CURRENT APPLICATION NUMBER: US/10/822,254

CURRENT FILING DATE: 2004-04-09

PRIOR APPLICATION NUMBER: US 60/461,787

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mine

PRIOR FILING DATE: 2003-04-10  
 PRIOR APPLICATION NUMBER: US 60/547,265  
 PRIOR FILING DATE: 2004-02-24  
 NUMBER OF SEQ ID NOS: 18  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 6  
 LENGTH: 109  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-822-254-6

Query Match 100.0%; Score 541; DB 34; Length 109;  
 Best Local Similarity 99.1%; Pred. No. 3.8e-59; Indels 0; Gaps 0;  
 Matches 109; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLKLKSVGAQDVTMKEVLFLGQYIMTRLYDEKQHIVH 60  
 Db 1 SQIPASEQETLVRPKPLKLKSVGAQDVTMKEVLFLGQYIMTRLYDEKQHIVH 60

Qy 61 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVYNNQQESSDSGTYSSEN 109  
 Db 61 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVYNNQQESSDSGTYSSEN 109

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**RESULT 2**  
 US-10-822-254-10  
 GENERAL INFORMATION: Application US/108222254  
 APPLICANT: Taremi, S S  
 APPLICANT: Xie, Gaolian  
 APPLICANT: Hesson, Thomas E  
 APPLICANT: Duka, Jose S  
 APPLICANT: Strickland, Corey  
 APPLICANT: Windsor, William  
 APPLICANT: Madison, Vincent  
 APPLICANT: Zhang, Rumin  
 APPLICANT: Reichert, Paul  
 TITLE OF INVENTION: Soluble, Stable Form of Hdm2, Crystalline Forms Thereof and Method  
 FILE REFERENCE: JB06017US01  
 CURRENT APPLICATION NUMBER: US/10/822,254  
 CURRENT FILING DATE: 2004-04-09  
 PRIOR APPLICATION NUMBER: US 60/461,787  
 PRIOR FILING DATE: 2003-04-10  
 PRIOR APPLICATION NUMBER: US 60/547,265  
 PRIOR FILING DATE: 2004-02-24  
 NUMBER OF SEQ ID NOS: 18  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 10  
 LENGTH: 109  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-822-254-10

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 Matches 108; Conservative 1; Mismatches 0; Gaps 0;

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 Db 1 SQIPASEQETLVRPKPLKLKSVGAQDVTMKEVLFLGQYIMTRLYDEKQHIVH 60

Qy 61 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVYNNQQESSDSGTYSSEN 109  
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**RESULT 3**  
 US-09-791-537-88970  
 Sequence 88970, Application US/09791537  
 GENERAL INFORMATION:  
 APPLICANT: Bionomix, Inc.  
 APPLICANT: Debe, Derek

RESULT 5  
 US-09-74-676-50031  
 Sequence 50031, Application US/09724676

GENERAL INFORMATION:  
 APPLICANT: Compugen LTD  
 TITLE OF INVENTION: Variants of alternative splicing  
 FILE REFERENCE: 129181.4 CompuGen  
 CURRENT APPLICATION NUMBER: US/09/724,676  
 CURRENT FILING DATE: 2000-11-28  
 NUMBER OF SEQ ID NOS: 97222  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 50031  
 LENGTH: 138  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-724-676-50031

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 Query 61 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNVQESSSDSGTYSSEN 109  
 Database 77 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNVQESSSDSGTYSSEN 125  
 SEQ ID NO 50032  
 LENGTH: 138  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-724-676-50032

RESULT 6  
 US-09-724-676-50032  
 GENERAL INFORMATION:  
 APPLICANT: Compugen LTD  
 TITLE OF INVENTION: Variants of alternative splicing  
 FILE REFERENCE: 129181.4 CompuGen  
 CURRENT APPLICATION NUMBER: US/09/724,676  
 CURRENT FILING DATE: 2000-11-28  
 NUMBER OF SEQ ID NOS: 97222  
 SOFTWARE: PatentIn version 3.2  
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 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-724-676-50032

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 Best Local Similarity 99.1%; Pred. No. 2.9e-58;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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 Query 61 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNVQESSSDSGTYSSEN 109  
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 SEQ ID NO 50032  
 LENGTH: 138  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-724-676-50032

RESULT 7  
 US-09-724-676-50031  
 GENERAL INFORMATION:  
 APPLICANT: Compugen LTD  
 TITLE OF INVENTION: Variants of alternative splicing  
 FILE REFERENCE: 129181.4 CompuGen  
 CURRENT APPLICATION NUMBER: US/09/724,676A  
 CURRENT FILING DATE: 2000-11-28  
 NUMBER OF SEQ ID NOS: 97222  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 50031  
 LENGTH: 138  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-724-676-50031

Query Match 98.9%; Score 548; DB 21; Length 209;  
 Best Local Similarity 99.1%; Pred. No. 5.1e-58;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO 1 SQIPASEQETLVRPKPLKLLKLSVGAQDVTMKEVLFLYQYIMTRLYDEKQHIVH 60  
 SEQ ID NO 23 SQIPASEQETLVRPKPLKLLKLSVGAQDVTMKEVLFLYQYIMTRLYDEKQHIVY 82  
 Query 61 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNVQESSSDSGTYSSEN 109  
 Database 83 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNVQESSSDSGTYSSEN 131  
 SEQ ID NO 50031  
 LENGTH: 138  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-724-676-50031

RESULT 8  
 US-09-724-676A-50032  
 GENERAL INFORMATION:  
 APPLICANT: Compugen LTD  
 TITLE OF INVENTION: Variants of alternative splicing  
 FILE REFERENCE: 129181.4 CompuGen  
 CURRENT APPLICATION NUMBER: US/09/724,676A  
 CURRENT FILING DATE: 2000-11-28  
 NUMBER OF SEQ ID NOS: 97222  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 50032  
 LENGTH: 138  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-724-676A-50032

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 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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 SEQ ID NO 17 SQIPASEQETLVRPKPLKLLKLSVGAQDVTMKEVLFLYQYIMTRLYDEKQHIVY 76  
 Query 61 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNVQESSSDSGTYSSEN 109  
 Database 77 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNVQESSSDSGTYSSEN 125  
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 LENGTH: 138  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-724-676A-50032

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 SEQ ID NO 17 SQIPASEQETLVRPKPLKLLKLSVGAQDVTMKEVLFLYQYIMTRLYDEKQHIVY 76  
 Query 61 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNVQESSSDSGTYSSEN 109  
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 ORGANISM: Homo sapiens  
 US-09-724-676A-50032

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 SEQ ID NO 23 SQIPASEQETLVRPKPLKLLKLSVGAQDVTMKEVLFLYQYIMTRLYDEKQHIVY 82  
 Query 61 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNVQESSSDSGTYSSEN 109  
 Database 83 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNVQESSSDSGTYSSEN 131  
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 LENGTH: 138  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-724-676A-50031

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Sequence 50030, Application US/09724676A  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181\_4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676A  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE ID NO: 50030  
LENGTH: 209  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676A-50030

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Query 61 CSNDLGLDFGVPSFSVKEHRKITYTMVNLVWNQOESSSDGTSVSEN 109  
Db 83 CSNDLGLDFGVPSFSVKEHRKITYTMVNLVWNQOESSSDGTSVSEN 131

RESULT 11  
US-10-990-328-10898  
Sequence 10898, Application US/10990328  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele  
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES  
ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND  
USES THEREOF  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: CJO01495  
CURRENT APPLICATION NUMBER: US/10/990,328  
CURRENT FILING DATE: 2004-11-17  
NUMBER OF SEQ ID NOS: 558824  
SEQ ID NO: 10898  
LENGTH: 253  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-990-328-10898

Query Match 98.9%; Score 548; DB 35; Length 253;  
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Db 23 SQIPASEQETLVRPKPLILKLUKSVAQDVTMKEVLFYLGQYIMTRLYDEKQHIVY 82

Query 61 CSNDLGLDFGVPSFSVKEHRKITYTMVNLVWNQOESSSDGTSVSEN 109  
Db 83 CSNDLGLDFGVPSFSVKEHRKITYTMVNLVWNQOESSSDGTSVSEN 131

RESULT 12  
US-60-505-218-571  
Sequence 571, Application US/60505218  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
CANCER, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CJO01482  
CURRENT APPLICATION NUMBER: US/60/505,218  
CURRENT FILING DATE: 2003-09-24

Query Match 98.9%; Score 548; DB 37; Length 253;  
Best Local Similarity 99.1%; Pred. No. 6.6e-58; Indels 0; Gaps 0;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query 1 SQIPASEQETLVRPKPLILKLUKSVAQDVTMKEVLFYLGQYIMTRLYDEKQHIVH 60  
Db 23 SQIPASEQETLVRPKPLILKLUKSVAQDVTMKEVLFYLGQYIMTRLYDEKQHIVY 82

Query 61 CSNDLGLDFGVPSFSVKEHRKITYTMVNLVWNQOESSSDGTSVSEN 109  
Db 83 CSNDLGLDFGVPSFSVKEHRKITYTMVNLVWNQOESSSDGTSVSEN 131

RESULT 15  
US-60-505-218-571  
Sequence 571, Application US/60505218  
GENERAL INFORMATION:  
APPLICANT: St. Jude Children's Research Hospital, Inc.  
APPLICANT: Kriwacki, Richard  
APPLICANT: Bothmer, Brian  
APPLICANT: Lewis, William  
TITLE OF INVENTION: Ars and Hdm2 Interaction Domains and  
Title of Invention: Method of Use Thereof  
FILE REFERENCE: 4415B/243642  
CURRENT APPLICATION NUMBER: PCT/US02/29780  
CURRENT FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: US 09/956,425  
PRIOR FILING DATE: 2001-09-19  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 8  
LENGTH: 491

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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29780-8

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Db    17 SQIPASQETLYRKPKPLKLKLSVGAQKDTYTMKEVLFYLQGYIMTKRLYDEKQHIVY 76
Qy   61 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNNQOBSSDSGTSYSEN 109
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RESULT 15
PCT-US03-12946-2602
; Sequence 2602, Application PC/TU0312946
; GENERAL INFORMATION: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: PRY, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: LY, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000150
; CURRENT APPLICATION NUMBER: PCT/US03/12946
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,827
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patentin version 3.2
; SEQ ID NO: 2602
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-12946-2602

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Query Match      98.9%;  Score 548;  DB 1;  Length 491;
Best Local Similarity 99.1%;  Pred. No. 1.6e-57;
Matches 108;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;
Qy   1 SQIPASQETLYRKPKPLKLKLSVGAQKDTYTMKEVLFYLQGYIMTKRLYDEKQHIVH 60
Db    17 SQIPASQETLYRKPKPLKLKLSVGAQKDTYTMKEVLFYLQGYIMTKRLYDEKQHIVY 76
Qy   61 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNNQOBSSDSGTSYSEN 109
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Search completed: February 16, 2005, 08:36:52  
Job time : 498 secs

*"THIS PAGE BLANK (USPTO)*

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OM protein - protein search, using sw model

Run on: February 16, 2005, 08:24:14 ; Search time 84 Seconds  
(without alignments)

51.028 Million cell updates/sec

Title: US-10-822-254-6

Perfect score: 554

Sequence: 1 SQIPASEQBTLYVRPKPLIKK.....NLVNVNQESSSDGTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 154980 seqs, 39324206 residues

Total number of hits satisfying chosen parameters: 154980

Minimum DB seq length: 0 ..

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_AA, New:  
1: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB\_pep:  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB\_pep:  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB\_pep:  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB\_pep:  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB\_pep:  
6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB\_pep:  
7: /cgn2\_6/ptodata/2/paa/US11\_NEW\_COMB\_pep:  
8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB\_pep:  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	311.5	56.2	205	6 US-10-450-763-60317	Sequence 60317, A
2	246	44.4	140	6 US-10-499-352A-580	Sequence 580, APP
3	246	44.4	148	6 US-10-499-352A-585	Sequence 585, APP
4	246	44.4	343	6 US-10-499-352A-584	Sequence 581, APP
5	225	40.6	107	6 US-10-499-352A-581	Sequence 581, APP
6	184	33.2	361	6 US-10-499-352A-583	Sequence 60315, A
7	176	31.8	243	6 US-10-450-763-60315	Sequence 60316, A
8	161	29.1	74	6 US-10-450-763-60316	Sequence 60316, A
9	75	13.5	254	6 US-10-450-763-60313	Sequence 60313, A
10	74.5	13.4	236	1 PCT-IB03-06519-5659	Sequence 5659, APP
11	73.5	13.3	621	6 US-10-450-763-55457	Sequence 55457, A
12	71	12.8	473	8 US-60-643-717-5118	Sequence 5118, APP
13	71	12.8	473	8 US-60-643-717-15655	Sequence 15655, A
14	70.5	12.7	787	6 US-10-450-763-55458	Sequence 55458, A
15	69	12.5	291	7 US-11-031-175-15646	Sequence 15646, A
16	66.5	12.0	422	8 US-60-643-717-23308	Sequence 23308, APP
17	66	11.9	2228	6 US-10-450-763-39401	Sequence 39401, A
18	66	11.9	2275	6 US-10-489-448-1766	Sequence 1766, APP
19	64	11.6	488	1 PCT-US04-20180-30	Sequence 30, APP
20	64	11.6	971	6 US-10-450-763-36645	Sequence 36645, A
21	63.5	11.5	598	6 US-10-450-763-52598	Sequence 52598, A
22	63	11.4	435	6 US-10-450-763-39488	Sequence 39488, A
23	63	11.4	533	6 US-10-450-763-39487	Sequence 39487, A
24	62.5	11.3	355	8 US-60-643-717-12981	Sequence 12981, A
25	62.5	11.3	445	6 US-10-450-763-45047	Sequence 45047, A

RESULT 1  
US-10-450-763-60317  
; Sequence 60317, Application US/10450763  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; CURRENT APPLICATION NUMBER: US/10-450-763  
; PRIORITY APPLICATION NUMBER: PCT/US03/08631  
; PRIORITY FILING DATE: 2003-06-11  
; PRIORITY APPLICATION NUMBER: 09/540,217  
; PRIORITY FILING DATE: 2000-03-31  
; PRIORITY APPLICATION NUMBER: 09/649,167  
; PRIORITY FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SEQ ID NO: 60317  
; LENGTH: 205  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (133)..(194)  
; OTHER INFORMATION: P53-associated protein (MDM2) domain identified by PFam, E-value=7.2e-47, PFam score of 169.1  
US-10-450-763-60317

Query Match 56.2%; Score 311.5; DB 6; Length 205;  
Best Local Similarity 73.9%; Pred. No. 2.5e-29;  
Matches 68; Conservative 9; Mismatches 9; Gaps 3;

Qy 1 SQIPASEQBTLYVRPKPLIKK.....NLVNVNQESSSDGTSVSEN 60  
Db 120 SQIPASEQBTLYVRPKPLIKK.....NLVNVNQESSSDGTSVSEN 179

Qy 61 -CSNDLJGDJFGVPFSVKERKITYMTIYRN 91  
Db 180 DCAN----LFPLVDISIRE--LYISNYITL 203

RESULT 2  
US-10-499-353A-580  
; Sequence 580, Application US/10499353A  
; GENERAL INFORMATION:  
; APPLICANT: diaDexus, Inc.  
; APPLICANT: Sun, Yongming  
; APPLICANT: Liu, Chenghua

TITLE OF INVENTION: Compositions and Methods Relating to Endometrial Specific Genes a  
 FILE REFERENCE: DEX-0377  
 CURRENT APPLICATION NUMBER: US/10/499,353A  
 PRIOR APPLICATION NUMBER: US 60/342,751  
 PRIOR FILING DATE: 2004-06-17  
 PRIORITY NUMBER: US 60/342,751  
 PRIOR FILING DATE: 2001-12-21  
 NUMBER OF SEQ ID NOS: 666  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 580  
 LENGTH: 140  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-10-499-353A-580

Query Match 44.4%; Score 246; DB 6; Length 140;  
 Best Local Similarity 55.4%; Pred. No. 8.3e-22;  
 Matches 46; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

Qy 12 VRPKPLKLKLSVGAQDVTYTMKEVLFYLGQYIMTKRLYDEKQHIVHCNSNDLIGDLFG 71  
 Db 27 VRPKPLKLHAAAGAQGEMFTVKEMHLYCQYIMVKLYDQEQSHMVYCGDLIGELLG 86

Qy 72 VPSFSVKERKLYTMYRNLYVV 94  
 Db 87 RQSFSVKDPSPLYDMRLRNLYVTI 109

RESULT 5  
 US-10-499-353A-581

Sequence 581, Application US/10499353A  
 GENERAL INFORMATION:  
 APPLICANT: diadexus, Inc.  
 APPLICANT: Sun, Yongming  
 APPLICANT: Liu, Chenghua  
 TITLE OF INVENTION: Compositions and Methods Relating to Endometrial Specific Genes a  
 FILE REFERENCE: DEX-0377  
 CURRENT APPLICATION NUMBER: US/10/499,353A  
 PRIOR APPLICATION NUMBER: US 60/342,751  
 PRIOR FILING DATE: 2004-06-17  
 NUMBER OF SEQ ID NOS: 666  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 581  
 LENGTH: 107  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-10-499-353A-581

Query Match 40.6%; Score 225; DB 6; Length 107;  
 Best Local Similarity 57.5%; Pred. No. 1.8e-19;  
 Matches 42; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Qy 12 VRPKPLKLKLSVGAQDVTYTMKEVLFYLGQYIMTKRLYDEKQHIVHCNSNDLIGDLFG 71  
 Db 27 VRPKPLKLHAAAGAQGEMFTVKEMHLYCQYIMVKLYDQEQSHMVYCGDLIGELLG 86

Qy 72 VPSFSVKERKLY 84  
 Db 87 RQSFSVKDPSFLY 99

RESULT 6  
 US-10-450-763-60315

Sequence 60315, Application US/10450763  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
 FILE REFERENCE: 790C13/US  
 CURRENT APPLICATION NUMBER: US/10/450,763  
 CURRENT FILING DATE: 2003-06-11  
 PRIOR APPLICATION NUMBER: PCT/US01/08631  
 PRIOR FILING DATE: 2001-03-30  
 PRIOR APPLICATION NUMBER: 09/540,217  
 PRIOR FILING DATE: 2000-03-31

RESULT 4  
 US-10-499-353A-584  
 Sequence 584, Application US/10499353A  
 GENERAL INFORMATION:  
 APPLICANT: diadexus, Inc.  
 APPLICANT: Sun, Yongming  
 APPLICANT: Liu, Chenghua  
 TITLE OF INVENTION: Compositions and Methods Relating to Endometrial Specific Genes a  
 FILE REFERENCE: DEX-0377

PRIOR APPLICATION NUMBER: 09/649,167  
 PRIOR FILING DATE: 2000-08-23  
 NUMBER OF SEQ ID NOS: 60736  
 SOFTWARE: Custom  
 SEQ ID NO: 60315  
 LENGTH: 361  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE: DOMAIN  
 NAME/KEY: (232)..(261)  
 LOCATION: OTHER INFORMATION: Zn-finger in Ran binding protein and other domain identified by PFam, accession name zf-RanBP, E-value=3.6e-08, pFam score of 40.6  
 OTHER INFORMATION: US-10-450-763-60315

Query Match Score 184; DB 6; Length 361;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-14;  
 Matches 38; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 SQIPASQETLVPRPKPLKLKLSVGAQKDYYTMKEVL 38  
 Db 120 SQIPASQETLVPRPKPLKLKLSVGAQKDYYTMKEVL 157

RESULT 7  
 US-09-786-702-2  
 GENERAL INFORMATION:  
 APPLICANT: Luke et al.  
 TITLE OF INVENTION: PIPERIZINE-4-PHENYL DERIVATIVES AS INHIBITORS OF THE INTERACTION BETWEEN MDM2 AND P 53  
 FILE REFERENCE: ASZD-P01-385  
 CURRENT APPLICATION NUMBER: US/03/786,702  
 CURRENT FILING DATE: 2001-03-07  
 PRIOR APPLICATION NUMBER: 9819860.9  
 PRIOR FILING DATE: 1998-09-12  
 NUMBER OF SEQ ID NOS: 3  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 2  
 LENGTH: 243  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-786-702-2

Query Match Score 176; DB 5; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-13;  
 Matches 36; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 SQIPASQETLVPRPKPLKLKLSVGAQKDYYTMKE 36  
 Db 17 SQIPASQETLVPRPKPLKLKLSVGAQKDYYTMKE 52

RESULT 8  
 US-10-450-763-60316  
 General Information:  
 APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
 CURRENT APPLICATION NUMBER: US/10/450,763  
 CURRENT FILING DATE: 2003-06-11  
 PRIOR APPLICATION NUMBER: PCT/CIP/US01/08631  
 PRIOR FILING DATE: 2001-03-30  
 PRIOR APPLICATION NUMBER: 09/540,217  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 09/649,167  
 PRIOR FILING DATE: 2000-08-23  
 NUMBER OF SEQ ID NOS: 60736  
 SOFTWARE: Custom  
 SEQ ID NO: 60316  
 LENGTH: 74

Query Match Score 161; DB 6; Length 74;  
 Best Local Similarity 80.9%; Pred. No. 4.1e-12;  
 Matches 38; Conservative 1; Mismatches 6;  
 Indels 2; Gaps 2;

Qy 1 SQIPASQETLVPRPKPLKLKLSVGAQKDYYTMKEVLFLGQYI 45  
 Db 21 SQIPASQETLVPRPKPLKLKLSVGAQKDYYCKRFENLQYI 67

RESULT 9  
 US-10-450-763-60313  
 Sequence 60313, Application US/10450763  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
 CURRENT APPLICATION NUMBER: US/10/450,763  
 CURRENT FILING DATE: 2003-06-11  
 PRIOR APPLICATION NUMBER: PCT/US01/08631  
 PRIOR FILING DATE: 2001-03-30  
 PRIOR APPLICATION NUMBER: 09/540,217  
 PRIOR FILING DATE: 2000-03-31  
 NUMBER OF SEQ ID NOS: 60736  
 SOFTWARE: Custom  
 SEQ ID NO: 60313  
 LENGTH: 254  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)...(254)  
 OTHER INFORMATION: Xaa = X or \* as defined in Table 2  
 US-10-450-763-60313

Query Match Score 75; DB 6; Length 254;  
 Best Local Similarity 29.0%; Pred. No. 0.24;  
 Matches 40; Conservative 12; Mismatches 34; Indels 52; Gaps 7;

Qy 1 SQIPASQETLYR-----PKPLI-----KLKSVGAQKDYYTMKEV----- 37  
 Db 120 SQIPASQETLYRQESEDYSQPLXILVALFTAAKKKKSLIKKKPKK-TKKRQVNLYCPLMP 178  
 Qy 38 -----LFLYLGQYIMTKRLYDEKQHQH-----IVHCSNDLJLGLFGVP 73  
 Db 179 LNLVKFKVVDLKMQVALMSAKODILNPALHDALKRKPKCPVCQRHNSND-CANLFPLV 237  
 Qy 74 SFSVKEHRKTYTMIVRNL 91  
 Db 238 DLSIRE-----LYISNNITL 252

RESULT 10  
 PCT/IB03-06509-5659  
 Sequence 5659, Application PC/TIB0306509  
 GENERAL INFORMATION:  
 APPLICANT: Regents of the University of Minnesota and The United States of America  
 TITLE OF INVENTION: Mycobacterial Diagnostics  
 CURRENT APPLICATION NUMBER: 09531/112/R01  
 CURRENT FILING DATE: 2003-03-06  
 PRIOR APPLICATION NUMBER: PCT/IB03/06509  
 PRIOR FILING DATE: 2003-03-06  
 PRIOR APPLICATION NUMBER: 10/137,113  
 PRIOR FILING DATE: 2002-04-30  
 PRIOR APPLICATION NUMBER: 60/362,396  
 PRIOR FILING DATE: 2002-03-06  
 NUMBER OF SEQ ID NOS: 5809  
 SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5659  
 LENGTH: 236  
 TYPE: PRT  
 ORGANISM: Mycobacterium paratuberculosis  
 PCT-IB03-06509-5659

Query Match 13.4%; Score 74.5; DB 1; Length 236;  
 Best Local Similarity 30.6%; Pred. No. 0.25;  
 Matches 19; Conservative 25; Mismatches 5; Gaps 3;

Qy 25 VGAQKDTYTMKEVLFYLGVQIMTKRLYDEKQHIVHC--SNDLIGDLFGVPS-FSVKER 81  
 Db 8 VGPPEDRYAMMDAAYVGLSAAQR--REFEQHMAHCRGCREAVADISGPALLSLRID 65

Qy 82 KI 83  
 Db 66 EV 67

RESULT 13  
 US-10-450-763-55457  
 Sequence 55457, Application US/10450763  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
 FILE REFERENCE: 790CIP3 US  
 CURRENT APPLICATION NUMBER: US/10/450,763  
 CURRENT FILING DATE: 2003-06-11  
 PRIOR APPLICATION NUMBER: PCT/US01/08631  
 PRIOR FILING DATE: 2001-03-10  
 PRIOR APPLICATION NUMBER: 09/540,217  
 PRIOR FILING DATE: 2000-03-31  
 SEQ ID NO 55457  
 LENGTH: 621  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-450-763-55457

Query Match 13.3%; Score 73.5; DB 6; Length 621;  
 Best Local Similarity 27.1%; Pred. No. 1;  
 Matches 29; Conservative 15; Mismatches 34; Indels 29; Gaps 4;

Qy 1 SQIPASEQ---ETLVRPKPLKKLKLSVG--AQKDTYTMKEVLFYLGVQIMTKRLYDE 53  
 Db 424 STVLASVORGIAEQQMENEPQFSAIMQAFGQSPFLQPDHLFLCNLFTLNTKQLXHK 483

Query Match 13.3%; Score 73.5; DB 6; Length 621;  
 Best Local Similarity 27.1%; Pred. No. 1;  
 Matches 29; Conservative 15; Mismatches 34; Indels 29; Gaps 4;

Qy 54 K-----QHQVHCSNDLIGDLFGVPSFSYKEHRIKTYM 86  
 Db 484 KIFRTAMLFLQEVNVLQVLVHKSHDLLQEIG----HRHSYNN 522

RESULT 12  
 US-10-643-717-5118  
 Sequence 5118, Application US/60643717  
 GENERAL INFORMATION:  
 APPLICANT: Abad, Mark S.  
 TITLE OF INVENTION: Genes and Uses for Plant Improvement  
 FILE REFERENCE: 38-21(53629)A  
 CURRENT APPLICATION NUMBER: US/60/643,717  
 CURRENT FILING DATE: 2005-01-12  
 NUMBER OF SEQ ID NOS: 19247  
 LENGTH: 473  
 TYPE: PRT  
 ORGANISM: Bacillus cereus ATCC 14579  
 US-60-643-717-5118

Query Match 12.8%; Score 71; DB 8; Length 473;  
 Best Local Similarity 22.8%; Pred. No. 1.5;  
 Matches 31; Conservative 22; Mismatches 37; Indels 46; Gaps 7;

Qy 9 ETLVRPKPLKKLKLSVG--KILKSVGAQKDTYTM--KEVLFYLGVQIMTKRLYDE 53  
 Db 248 ETLVRDKNGTIVTQAEEHNGENKEFKAKMLVSGRANTQNLGENTDIVVERG-YLTQTNEF 306

Query Match 12.8%; Score 71; DB 8; Length 473;  
 Best Local Similarity 22.8%; Pred. No. 1.5;  
 Matches 31; Conservative 22; Mismatches 37; Indels 46; Gaps 7;

Qy 51 YDEKQHIVHCSNDLIGDLFGVPSFSYKEHRIKTYM 86  
 Db 307 YQTKEESHI-YAIGDVTG--GLQLAHVASHEGTAEEHAGKEVTPIDYSMSVKCVYSSP 362

Query Match 12.8%; Score 71; DB 8; Length 473;  
 Best Local Similarity 22.8%; Pred. No. 1.5;  
 Matches 31; Conservative 22; Mismatches 37; Indels 46; Gaps 7;

Qy 92 ---VVVNQOESSSDG 103  
 Db 363 EVASVGLTEQBAEKKG 378

RESULT 14  
 US-10-450-763-55458  
 Sequence 55458, Application US/10450763  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
 FILE REFERENCE: 790CIP3/US  
 CURRENT APPLICATION NUMBER: US/10/450,763  
 CURRENT FILING DATE: 2003-06-11  
 PRIOR APPLICATION NUMBER: PCT/US01/08631  
 PRIOR FILING DATE: 2001-03-30  
 SEQ ID NO 55458  
 LENGTH: 787  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (424). (443)  
 OTHER INFORMATION: ADRESIN FAMILY SIGNATURE domain identified by eMATRIX,

OTHER INFORMATION: accession number PR00690A, p-value=9.86e-09, raw score of 10.86  
 US-10-450-763-53458

Query Match 12.7%; Score 70.5; DB 6; Length 787;  
 Best Local Similarity 25.5%; Pred. No. 3.1;  
 Matches 25; Conservative 19; Mismatches 33; Indels 21; Gaps 3;

Qy 1 SQTASSEQ---ETLVRPKPLILKLUKLSVG---AQKDVTMKEVLFYLGQYIMTKRLYDE 53  
 Db 598 SIVLASVQRGIAEBQMNEPQSAIMAGFSFLQPPIHLPQNLFYLETNTKQLYHK 657

Qy 54 K-----QHIVIVCISNDLJGDLEFGVPSESV 77  
 Db 658 KIFRTAMLFQFVNVLQGVLTVKSHDLIQQEIGIAINM 695

RESULT 15  
 US-11-031-175-15646

GENERAL INFORMATION:  
 APPLICANT: Goldman, Barry S.  
 APPLICANT: Hinkle, Gregory J.  
 APPLICANT: Slater, Steven C.  
 APPLICANT: Wiegard, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10 (15849) B

CURRENT APPLICATION NUMBER: US/11/031,175

CURRENT FILING DATE: 2005-01-08

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 15646

LENGTH: 291

TYPE: PRT

ORGANISM: Myxococcus xanthus

FEATURE:

NAME/KEY: unsure

LOCATION: (1) · (291)

OTHER INFORMATION: unsure at all Xaa locations

US-11-031-175-15646

Query Match 12.5%; Score 69; DB 7; Length 291;  
 Best Local Similarity 25.8%; Pred. No. 1.4;  
 Matches 23; Conservative 23; Mismatches 23; Indels 20; Gaps 6;

Qy 1 LVRPKPLILKLL--RSVGAQKDVTMKEVLFYLGQYIMTKRLYDEQHQHIVCSNDLIG 67  
 Db 100 LTRYPPPLSPVLYHGRLTGAR-----MKVNAFMGPVTLPEDV-EERTEVVH---LVA 148

Qy 68 DLFGVPSFSVKB--HRKI---YTMYRN 90  
 Db 149 GSGAVPNFAIKDMLHKGKRTHTFLSN 177

Search completed: February 16, 2005, 08:38:20  
 Job time : 84 secs

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OM protein - protein search, using sw model

Run on: February 16, 2005, 08:21:05 ; Search time 166 Seconds  
 (without alignments)  
 253.957 Million cell updates/sec

Title: US-10-822-254-6

Perfect score: 554

Sequence: 1 SQIPASEQETLYVRPKPLIK. .... .NLVVVNQQESSSDSGTGSSEN 109

Scoring table: BL05062

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_16Dec04;\*

1: geneseqp1980B;\*

2: geneseqp1980B;\*

3: geneseqp2000B;\*

4: geneseqp2001B;\*

5: geneseqp2002B;\*

6: geneseqp2003A;\*

7: geneseqp2003B;\*

8: geneseqp2004S;\*

26 548 98.9 491 8 ADQ19417 Human sof  
 27 548 98.9 491 8 ADR58893 Human MDM  
 28 548 98.9 491 8 AAU32421 Novel hum  
 29 531.5 95.9 216 3 AAB08846 A human M  
 30 522.5 94.3 522 7 ADJ95152 Novel NOV  
 31 522.5 94.3 522 7 ADJ95154 Novel NOV  
 32 488.5 88.2 489 2 AAR42176 Murine MD  
 33 488.5 88.2 489 2 AAR76697 Mouse MDM  
 34 488.5 88.2 489 2 AAW07888 Murine MD  
 35 488.5 88.2 489 2 AAW15464 Murine MD  
 36 488.5 88.2 489 2 AAW48242 Mouse MDM  
 37 488.5 88.2 489 2 AAW57246 Mouse MDM  
 38 488.5 88.2 489 2 AAW42397 Amino aci  
 39 488.5 88.2 489 2 AAW42972 Amino aci  
 40 488.5 88.2 489 2 AAW94105 Mouse MDM  
 41 488.5 88.2 489 2 AAE25114 Mouse dou  
 42 488.5 88.2 489 5 ABB57099 Mouse isc  
 43 488.5 88.2 489 5 AAO15375 Mouse Dm2  
 44 488.5 88.2 489 7 ADD21816 Mouse mdm  
 45 488.5 88.2 489 7 ADE61560 Rat Prote

## ALIGNMENTS

## RESULT 1

AAR75494 standard; protein; 284 AA.

XX ID AAR75494;

AC AAR75494;

XX DT 02-PFB-1996 (first entry)

XX DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.

XX FH Human double minute gene 2; hdm-2; antibody binding region; antigen;

KW cancer; sarcoma; rhabdomyosarcoma; diagnosis; immunoassay.  
 XX OS Homo sapiens.XX Key Location/Qualifiers  
 1..284 /note= "amino acids 1-284 of hdm-2 gene product"

## SUMMARIES

XX DE4339533-A1.

XX PN

XX XX

XX PD 14-JUN-1995.

XX PF 19-NOV-1993;

XX PR 19-NOV-1993;

XX PA (DEKRR-) DEUT FRIEBSFORSCHUNGSZENTRUM.

XX PI Zentgraf H, Klein R, Frey M, Martens R;

XX XX

XX WPI 1995-216248/29.

XX DR N-PSB; ARQ2315.

XX Detection of human double minute gene 2 (hdm-2) antibodies - by incubation with new hdm-2 or antibody-binding hdm-2 fragments; useful in the detection of specific cancers.

XX PS Claim 1; Fig 1; 12pp; German.

XX Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human double minute 2) gene product are claimed. The overlapping protein fragments contain binding regions for hdm-2-specific antibodies and are useful for identifying such antibodies in a claimed immunoassay method. The presence of anti-hdm-2 antibodies is diagnostic of certain forms of cancer, e.g. rhabdomyosarcoma

XX Sequence 284 AA;

SQ

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Match Length DB ID Description

Result No.	Score	Match	Length	DB	ID	Description
1	548	98.9	284	2	AAR75494	Aar75494 Human dou
2	548	98.9	284	2	AAR75397	Aar7397 Human dou
3	548	98.9	491	2	AAR42175	Aar42175 Human MDM
4	548	98.9	491	2	AAR76696	Aar76696 Human MDM
5	548	98.9	491	2	AAW07887	Aaw07887 Human MDM
6	548	98.9	491	2	AAW15463	Aaw15463 Human MDM
7	548	98.9	491	2	AAW13380	Aaw13380 Human MDM
8	548	98.9	491	2	AAW13600	Aaw13600 Murine do
9	548	98.9	491	2	AAW48241	Aaw48241 Human MDM
10	548	98.9	491	2	AAM57241	Aam57241 Human MDM
11	548	98.9	491	2	AAW42879	Aaw42879 Amino aci
12	548	98.9	491	2	AAW42971	Aaw42971 Amino aci
13	548	98.9	491	2	AAM94304	Aam94304 Human MDM
14	548	98.9	491	3	AAV96567	Aav96567 MDM2 onco
15	548	98.9	491	4	AAB48284	Aab48284 Human MDM
16	548	98.9	491	5	AAB2654	Aab2654 Human Rin
17	548	98.9	491	5	AAB22698	Aab22698 Human Rin
18	548	98.9	491	5	AAB25913	Aab25913 Human dou
19	548	98.9	491	5	AAO15376	Aao15376 Human Dm2
20	548	98.9	491	7	ADD21815	Add21815 Human Pro
21	548	98.9	491	7	ADE61562	Ade61562 Human Pro
22	548	98.9	491	8	ADD23893	Add23893 Human E3
23	548	98.9	491	8	ADG052353	Ado52353 Human p53
24	548	98.9	491	8	ADP12593	Adp12593 Protein e
25	548	98.9	491	8	ADN71936	Adn71936 NMD2 prot

Query Match 98.9%; Score 548; DB 2; Length 284;  
 Best Local Similarity 99.1%; Pred. No. 3\_2e-64;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLIKLKSVGAQDFTYTMKEVLFLYLGQYIMTRKLYDEKQHIVH 60  
 Db 17 SQIPASEQETLVRPKPLIKLKSVGAQDFTYTMKEVLFLYLGQYIMTRKLYDEKQHIVV 76

Qy 61 CSNDLGLPGLFGVPFSVKEHRKLYTMIYRNLYVNNQESSSDSGTSVSEN 109  
 Db 77 CSNDLGLPGLFGVPFSVKEHRKLYTMIYRNLYVNNQESSSDSGTSVSEN 125

**RESULT 2**  
 ARR75397 standard; protein; 284 AA.  
 ID AAR75397  
 AC AAR75397;  
 XX DT 25-MAR-2003 (revised)  
 DT 25-JAN-1996 (First entry)  
 DB Human double minute 2 (hdm-2) antibody-binding region fragment 1.  
 XX Human double minute gene 2; hdm-2; antibody binding region; antigen;  
 KW cancer; barcoma; rhabdomyosarcoma; diagnosis.  
 XX OS Homo sapiens.  
 FH Key Location/Qualifiers  
 Region 1..284  
 FT /note= "amino acids 1-284 of hdm-2 gene product"  
 XX PN DE4345249-A1.  
 XX PD 24-MAY-1995.  
 XX PR 19-NOV-1993; 93DE-04345249.  
 XX PA (DEUR-) DEUT KRBSFORSCHUNGSZENTRUM.  
 XX PI Zentgraf H, Klein R, Frey M, Martens R;  
 XX DR WPI: 1995-195167/26.  
 XX DR N-PSDB; AAQ87261.  
 PT New hdm-2 fragments contg. antibody binding region - used to detect  
 PT specific antibodies for diagnosis of cancers, also new DNA sequences  
 PT encoding them.  
 XX PS Claim 2; Fig 1; 11pp; German.  
 XX CC Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human  
 CC double minute 2) gene product are claimed. The overlapping protein  
 CC fragments contain binding regions for hdm-2 specific antibodies and are  
 CC useful for identifying such antibodies. The presence of anti-hdm-2  
 CC antibodies is diagnostic of certain forms of cancer, e.g.  
 CC rhabdomyosarcoma. (Updated on 25-MAR-2003 to correct PF field.)  
 XX SQ Sequence 284 AA:  
 CC Query Match 98.9%; Score 548; DB 2; Length 491;  
 CC Best Local Similarity 99.1%; Pred. No. 7e-64;  
 CC Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLIKLKSVGAQDFTYTMKEVLFLYLGQYIMTRKLYDEKQHIVH 60  
 Db 17 SQIPASEQETLVRPKPLIKLKSVGAQDFTYTMKEVLFLYLGQYIMTRKLYDEKQHIVV 76

Query Match 98.9%; Score 548; DB 2; Length 284;  
 Best Local Similarity 99.1%; Pred. No. 3\_2e-64;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 61 CSNDLGLPGLFGVPFSVKEHRKLYTMIYRNLYVNNQESSSDSGTSVSEN 109  
 Db 77 CSNDLGLPGLFGVPFSVKEHRKLYTMIYRNLYVNNQESSSDSGTSVSEN 125

**RESULT 4**  
 AAR76696 standard; protein; 491 AA.  
 ID AAR76696

XX AAR76696; FT Modified-site 166..169  
 XX label= "phosphorylation\_site" /label= "potential casein\_kinase II phosphorylation site"  
 DT 16-OCT-2003 (revised) FT Binding-site 181..185  
 DT 01-NOV-1995 (first entry) FT  
 XX Human MDM2 Protein. FT Modified-site 192..195  
 DB Human MDM2 protein. FT  
 XX MDM2; barcoma; diagnostic; DNA probe. FT  
 XX OS Homo sapiens; (cell line Caco-2). FT  
 XX PN US5420263-A. FT  
 PD 30-MAY-1995. FT  
 XX PF 07-APR-1993; 93US-00044619. FT  
 XX PR 07-APR-1992; 92US-00867840. FT  
 PR 23-JUN-1992; 92US-00903103. FT  
 XX PA (UYJO ) UNIV JOHNS HOPKINS. FT  
 XX PI Vogelstein B, Kinzler KW; FT  
 XX DR WPI: 1995-206312/27. FT  
 DR N-PSDB; AAQ94589. FT  
 XX PT New human MDM2 cDNA - used to develop prods. for use in the diagnosis and PR 07-APR-1992; 92US-00867840.  
 PT treatment of tumours. PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619. PR  
 XX PS Claim 1; Col 23-26; 34pp; English. PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS. XX  
 CC The human MDM2 gene is genetically altered (i.e. amplified) in human tumour cells. The human MDM2 protein binds to human p53 and allows the cell to escape from p53-regulated growth. Detecting increased gene product expression (using probes, proteins, antibodies and inhibitors) allows diagnosis and therapy of cancers such as colorectal carcinoma, lung cancer and chronic myelogenous leukaemia. (Updated on 16-OCT-2003 to standardise OS field)  
 XX SQ Sequence 491 AA;  
 CC The human MDM2 gene is genetically altered (i.e. amplified) in human tumour cells. The human MDM2 protein binds to human p53 and allows the cell to escape from p53-regulated growth. Detecting increased gene product expression (using probes, proteins, antibodies and inhibitors) allows diagnosis and therapy of cancers such as colorectal carcinoma, lung cancer and chronic myelogenous leukaemia. (Updated on 16-OCT-2003 to standardise OS field)  
 XX SQ Query Match 98..9%; Score 548; DB 2; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7e-64; Gaps 0;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SQIPASEQETLYRKPKPLLKLSVGAQDVTMKEVLFLGQYIMTRKLYDEKQOHIVH 60  
 Db 17 SQIPASEQETLYRKPKPLLKLSVGAQDVTMKEVLFLGQYIMTRKLYDEKQOHIVY 76  
 Qy 61 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNNQESSSDSGTYSSEN 109  
 Db 77 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNNQESSSDSGTYSSEN 125  
 XX SQ Sequence 491 AA;  
 XX SQ Query Match 98..9%; Score 548; DB 2; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7e-64; Gaps 0;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SQIPASEQETLYRKPKPLLKLSVGAQDVTMKEVLFLGQYIMTRKLYDEKQOHIVH 60  
 Db 17 SQIPASEQETLYRKPKPLLKLSVGAQDVTMKEVLFLGQYIMTRKLYDEKQOHIVY 76  
 Qy 61 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNNQESSSDSGTYSSEN 109  
 Db 77 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVNNQESSSDSGTYSSEN 125  
 RESULT 5  
 ID AAW07887 standard; protein; 491 AA.  
 XX AC AAW07887;  
 XX DT 25-MAR-2003 (revised)  
 DT 28-JAN-1997 (first entry)  
 XX DB Human MDM-2, involved in tumour-development.  
 KW P53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;  
 KW antibody fusion protein; therapy.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 RESULT 6  
 ID AAW15463 standard; protein; 491 AA.  
 XX

AC AAW15463;  
 XX 25-MAR-2003; (revised)  
 DT 18-JUN-1997 (first entry)  
 DE Human MDM2.  
 XX Human; MDM2 protein; antibody; detection; cancer; diagnosis;  
 KW p53-regulated growth.  
 KW Homo sapiens.  
 OS XX  
 PN US5618921-A.  
 PA XX  
 PR 08-APR-1997.  
 XX FF 17-FEB-1995; 95US-00390479.  
 PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 PI Vogelstein B, Kinzler KW, Burrell M, Hill DE;  
 DR WPI; 1997-225474/20.  
 DR N-PSDB; AAT66410.  
 PT Antibodies specific for human MDM2 protein - for diagnosis of cancer.  
 PS XX  
 SQ Claim 1; Col 19-24; 35pp; English.  
 XX This sequence represents the human MDM2 protein. Antibodies that  
 CC specifically bind to human MDM2 protein may be used for detecting  
 CC elevated expression of the MDM2 gene in a human tissue or body fluid  
 CC sample, esp. for cancer diagnosis. The antibodies may be used to  
 CC interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear  
 CC to sequester p53 and allow the cell to escape from p53-regulated growth.  
 CC (Updated on 25-MAR-2003 to correct FF field.)  
 XX SQ Sequence 491 AA;  
 XX Query Match 98.9%; Score 548; DB 2; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7e-64;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SQIPASEQETLYVRPKPLIKLKSGVAQDVTMKEVLFLGQYIMTRKLYDEKQHQIVH 60  
 Db 17 SQIPASEQETLYVRPKPLIKLKSGVAQDVTMKEVLFLGQYIMTRKLYDEKQHQIVY 76  
 Qy 61 CSNDLIGDLFGVPSFSVKEHRKITYMIVRNLYVNQESSDSGTYSSEN 109  
 Db 77 CSNDLIGDLFGVPSFSVKEHRKITYMIVRNLYVNQESSDSGTYSSEN 125

RESULT 7  
 AAW13380  
 ID AAW13380 standard; protein; 491 AA.  
 AC AAW13380;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 05-JUN-1997 (first entry)  
 DE Human MDM2 protein.  
 KW Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;  
 KW elevation; expression; diagnosis; neoplasia; neoplastic transformation;  
 KW sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia.  
 KW OS Homo sapiens.

AC AAW13380;  
 XX PN US55606044-A.  
 PD 25-FEB-1997.  
 XX PP 17-FEB-1995; 95US-00390546.  
 PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 PI Kinzler KW, Vogelstein B, Hill DE, Burrell M;  
 DR WPI; 1997-15323/14.  
 DR N-PSDB; AAT62065.  
 XX PT Detection of amplification of human MDM2 gene - useful for diagnosis of  
 neoplasia or potential neoplastic transformation.  
 PS Example 1; Col 21-24; 35pp; English.  
 XX The present sequence is the human MDM2 protein, the cDNA for which was  
 CC isolated from a human CaCo-2 colonic carcinoma cell cDNA library using a  
 murine MDM2 cDNA probe. The MDM2 cDNA can be used as a probe to detect  
 CC the amplification or elevated expression of a human MDM2 gene, which is  
 CC diagnostic of neoplasia or the potential for neoplastic transformation,  
 CC useful for the detection of, e.g. sarcomas, colorectal carcinoma, lung  
 CC cancer and chronic myelogenous leukaemia. (updated on 25-MAR-2003 to  
 CC correct FF field.)  
 XX SQ Sequence 491 AA;  
 XX Query Match 98.9%; Score 548; DB 2; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7e-64;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SQIPASEQETLYVRPKPLIKLKSGVAQDVTMKEVLFLGQYIMTRKLYDEKQHQIVH 60  
 Db 17 SQIPASEQETLYVRPKPLIKLKSGVAQDVTMKEVLFLGQYIMTRKLYDEKQHQIVY 76  
 Qy 61 CSNDLIGDLFGVPSFSVKEHRKITYMIVRNLYVNQESSDSGTYSSEN 109  
 Db 77 CSNDLIGDLFGVPSFSVKEHRKITYMIVRNLYVNQESSDSGTYSSEN 125

RESULT 8  
 AAW13600  
 ID AAW13600 standard; protein; 491 AA.  
 AC AAW13600;  
 XX DT 16-JAN-1998 (first entry)  
 XX Murine double minute 2 protein sequence.  
 XX KW Mouse; Mdm2; murine double minute phosphoprotein; binding; modulation;  
 KW tumour suppressor; P53; oncogene; cell cycle arrest; p107; antagonist;  
 KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;  
 KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;  
 KW restenosis.  
 XX OS Mus musculus.  
 PN WO9709343-A2.  
 XX PD 13-MAR-1997.  
 PR 02-SEP-1996;  
 XX PR 04-SEP-1995; 95WO-FR001340.  
 XX PR 04-SEP-1995; 95FR-00010331.  
 PA (RHON ) RHONE POULENC RORER SA.

PA (INRM ) INST NAT SANTE & RECH MEDICALE.  
 XX DR WPI: 1998-239206/21.  
 PI DR N-PSDB; AAV2049.  
 XX Cancer diagnosis - by determination of MDM2 protein.

PT XX  
 XX  
 PT Treating cancer with antagonist of oncogenic activity of protein Mdm2 -  
 PT or nucleic acid encoding an antagonist, also viral vectors contg. this  
 PT nucleic acid.  
 XX  
 PS Claim 2; Page 26-30; 43pp; French.

CC This is the amino acid sequence of the mouse Mdm2 (murine double minute-  
 CC 2) protein, 90 kd phosphoprotein which binds and modulates the activity  
 CC of the tumour suppressor protein p53. It has now been shown that the mdm2  
 CC protein itself has oncogenic properties, especially in a p53-null  
 CC background. Mdm2 is observed to unblock cell cycle arrest in G1 caused by  
 CC over-expression of the p107 protein. This is especially done by the  
 CC region covering amino acid 1-134. The invention therefore relates to  
 CC antagonists able to inhibit the oncogenic activity of mdm2. These include  
 CC fragments of the p53 protein, especially amino acids 1-52, 1-41, 6-41, 16  
 CC -25 or 18-23 (AAW13602-6), or fragments of transcription factors e.g.  
 CC TBP1, TBP or TAF250, which bind amino acids 1-134 of mdm2. Other  
 CC antagonists include compounds which disrupt binding to region 135-491 of  
 CC mdm2, e.g. Rb, L5 or the transcription factor E2F. The antagonists are  
 CC used to treat e.g. adenocarcinoma of the breast, lung or stomach; myeloid leukaemia; B cell lymphoma, or other  
 CC hyperproliferative conditions such as restenosis  
 XX Sequence 491 AA;

Query Match 98.9%; Score 548; DB 2; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7e-64;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLKLLKSKVGAQKDVTMKEVLFLYQYIMTRLYDEKQHIVH 60  
 Db 17 SQIPASEQETLVRPKPLKLLKSKVGAQKDVTMKEVLFLYQYIMTRLYDEKQHIVY 76

Qy 61 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVVNQESSDSGTSVSEN 109  
 Db 77 CSNDLIGDLFGVPSFSVKEHRKITYMIRNLVVNQESSDSGTSVSEN 125

RESULT 9  
 AAW4241 ID AAW4241 standard; protein; 491 AA.  
 XX AC AAW4B241;  
 XX DT 18-JUN-1998 (first entry)  
 DE Human MDM2.  
 XX Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease;  
 KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 PN US5736338-A.  
 XX 07-APR-1998.  
 PD 07-APR-1998.  
 PP 17-FEB-1995; 95US-00390517.  
 XX PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 PI Vogelstein B, Kinzler KW,  
 XX Homo sapiens.  
 PN US5756455-A.  
 XX PD 26-MAY-1998.  
 XX PF 17-FBB-1995; 95US-00390515.  
 XX PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 PI Vogelstein B, Kinzler KW,  
 XX Homo sapiens.  
 PN US5756455-A.  
 XX PR Inhibiting growth of tumour cells having MDM2 gene amplification - with  
 PT p53 protein fragment.  
 XX PR 10-AUG-1998 (first entry)  
 DE Human MDM2.  
 XX Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease;  
 KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 PN US5736338-A.  
 XX 07-APR-1998.  
 PD 07-APR-1998.  
 PP 17-FEB-1995; 95US-00390517.  
 XX PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Vogelstein B, Kinzler KW, Hill DE, Burrell M;

RESULT 10  
 AAW57241 ID AAW57241 standard; protein; 491 AA.  
 XX AC AAW57241;  
 XX DT 10-AUG-1998 (first entry)  
 DE Human MDM2 protein.  
 XX Human; P53; MDM2; tumour; growth inhibition; amplification;  
 KW malignant fibrous histiocytoma; liposarcoma.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN US5756455-A.  
 XX PD 26-MAY-1998.  
 XX PF 17-FBB-1995; 95US-00390515.  
 XX PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 PI Vogelstein B, Kinzler KW,  
 XX Homo sapiens.  
 PN US5756455-A.  
 XX PR Inhibiting growth of tumour cells having MDM2 gene amplification - with  
 PT p53 protein fragment.  
 XX PR 10-AUG-1998 (first entry)  
 DE Human MDM2.  
 XX Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease;  
 KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 PN US5736338-A.  
 XX 07-APR-1998.  
 PD 07-APR-1998.  
 PP 17-FEB-1995; 95US-00390517.  
 XX PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Vogelstein B, Kinzler KW, Hill DE, Burrell M;

CLAIM 1: Col 23-28; 40pp; English.

XX DR N-PSDB; AAV28876.

XX PS Claim 1; Col 23-28; 40pp; English.

XX DR N-PSDB; AAV28876.

XX PS Inhibiting growth of tumour cells having MDM2 gene amplification - with  
 PT p53 protein fragment.

XX PR 10-AUG-1998 (first entry)  
 DE Human MDM2.  
 XX Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease;  
 KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 PN US5736338-A.  
 XX 07-APR-1998.  
 PD 07-APR-1998.  
 PP 17-FEB-1995; 95US-00390517.  
 XX PR 07-APR-1992; 92US-00867840.  
 PR 23-JUN-1992; 92US-00903103.  
 PR 07-APR-1993; 93US-00044619.  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Vogelstein B, Kinzler KW, Hill DE, Burrell M;

CC A method has been developed for inhibiting the growth of tumour cells  
 CC containing a human MDM2 gene amplification. The method comprises treating  
 CC the tumour cells with a DNA molecule that expresses a polypeptide capable  
 CC of binding to human MDM2 protein. The present sequence represents human  
 CC MDM2 protein. The present invention describes three preferred  
 CC polypeptides for binding human MDM2: (1) the polypeptide comprises amino

CC acids 1-50 of p53 (see AAW57240); (2) the polypeptide comprises amino acids 13-41 of p53 (see AAW57240) and at least nine additional p53 residues on the N- or C-terminal side, provided that the polypeptide lacks the homooligomerisation domain of p53; (3) the polypeptide comprises amino acids 13-41 of p53 (see AAW57241) and at least nine additional p53 residues on the N- or C-terminal side, provided that the polypeptide lacks amino acids 138-193 of p53. Some malignant fibrous histiocytomas and liposarcomas have an MDM2 gene amplification, so detection of increased expression of MDM2 gene products indicates tumorigenesis.

XX Sequence 491 AA;

Query Match 98.9%; Score 548; DB 2; Length 491;  
Best Local Similarity 99.1%; Pred. No. 7e-64;  
Matches 108; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLKLLKSVGAQKDVTMKEVLFTLGQYIMTRKLYDEKQHIVH 60  
Db 17 SQIPASEQETLVRPKPLKLLKSVGAQKDVTMKEVLFTLGQYIMTRKLYDEKQHIVY 76

XX RESULT 11

AAW42879 Standard; protein; 491 AA.  
ID AAW42879  
XX AC AAW42879;

XX DT 30-APR-1998 (first entry)  
DE Amino acid sequence of human MDM2.

XX MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;  
\* KW binding; tumour cell; p53-regulated growth; inhibition;  
KW anti-cancer agent.

XX Homo sapiens.

OS Homo sapiens.

XX PN US570136-A.

XX PD 13-JAN-1998.

XX PF 17-FEB-1995;

XX PR 07-APR-1992;

XX PR 23-JUN-1992;

XX PR 07-APR-1993;

XX PR 18-MAY-1994;

XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX XX PI Vogelstein B, Kinzler KW;

XX XX DR WPI: 1998-076411/07.

XX XX DR N-PSDB; AAV03507.

XX Cell containing reporter construct containing human MDM2 and p53 genes - Disclosure; Coulombs 22-28; 37pp; English.  
XX The present sequence represents human MDM2. The MDM2 gene is amplified in some human tumours. The amplification of this gene is diagnostic of neoplasia or its parent cell. It is speculated that the MDM2 protein is a potential DNA binding protein that functions in the modulation of expression of other genes and, when present in excess, interferes with normal constraints on cell growth. A cell containing three recombinant DNA constructs was produced. These constructs encode an MDM2 protein fused to a sequence-specific DNA binding domain, a p53 polypeptide fused to a transcriptional activation domain, and a reporter gene downstream from a DNA element which is recognised by the sequence-specific DNA-

CC binding domain. The cell is used to identify a compound which interferes CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour CC cells and since binding of MDM2 to p53 appears to allow tumour cells to escape from p53-regulated growth, compounds that inhibit such binding CC would be useful as anti-cancer agents.  
XX Sequence 491 AA;

SQ Query Match 98.9%; Score 548; DB 2; Length 491;  
Best Local Similarity 99.1%; Pred. No. 7e-64;  
Matches 108; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLKLLKSVGAQKDVTMKEVLFTLGQYIMTRKLYDEKQHIVH 60  
Db 17 SQIPASEQETLVRPKPLKLLKSVGAQKDVTMKEVLFTLGQYIMTRKLYDEKQHIVY 76

Qy 61 CSNDLIGDLFGVPSFSVKEHRKLYTMIYRNLYVNNQQESSSDSGTSVSEN 109  
Db 77 CSNDLIGDLFGVPSFSVKEHRKLYTMIYRNLYVNNQQESSSDSGTSVSEN 125

XX RESULT 12

AAW42971

ID AAW42971 standard; protein; 491 AA.

XX AC AAW42971;  
XX DT 29-APR-1998 (first entry)  
XX DB Amino acid sequence of human MDM2.

XX KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;  
KW binding; tumour cell; p53-regulated growth; inhibition;  
KW anti-cancer agent.

XX OS Homo sapiens.

XX PN US5702903-A.

XX XX PD 30-DEC-1997.

XX XX PP 13-NOV-1995; 95US-00557393.

XX XX PR 07-APR-1992; 92US-00857840.

XX XX PR 23-JUN-1992; 92US-00933103.

XX XX PR 07-APR-1993; 93US-0004619.

XX XX PR 18-MAY-1994; 94US-00245500.

XX XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX XX PI Vogelstein B, Kinzler KW;

XX XX DR WPI: 1998-076411/07.

XX XX DR N-PSDB; AAV03507.

XX Cell containing reporter construct containing human MDM2 and p53 genes - Disclosure; Coulombs 22-28; 37pp; English.  
XX The present sequence represents human MDM2. The MDM2 gene is amplified in some human tumours. The amplification of this gene is diagnostic of neoplasia or its parent cell. It is speculated that the MDM2 protein is a potential DNA binding protein that functions in the modulation of expression of other genes and, when present in excess, interferes with normal constraints on cell growth. A cell containing three recombinant DNA constructs was produced. These constructs encode an MDM2 protein fused to a sequence-specific DNA binding domain, a p53 polypeptide fused to a transcriptional activation domain, and a reporter gene downstream from a DNA element which is recognised by the sequence-specific DNA-

CC binding domain. The cell is used to identify a compound which interferes CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour CC cells and since binding of MDM2 to p53 appears to allow tumour cells to escape from p53-regulated growth, compounds that inhibit such binding CC would be useful as anti-cancer agents.  
XX Sequence 491 AA;

SQ Query Match 98.9%; Score 548; DB 2; Length 491;

Best Local Similarity 99.1%; Pred. No. 7e-64;  
Matches 108; Conservative 1; Mismatches 0; Gaps 0;

Page 7

cells and since binding of MDM2 to p53 appears to allow tumour cells to escape from p53-regulated growth, compounds that inhibit such binding would be useful as anti-cancer agents.

cells and since binding of MDM2 to p53 appears to allow tumour cells to escape from p53-regulated growth, compounds that inhibit such binding would be useful as anti-cancer agents	Sequence 491 AA;	Query Match	Score 548; DB 2; Length 491;	Best Local Similarity 98.9%; Pred. No. 7e-64;	Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Qy	1 SQIPASEQETLVRPKILLKLLKSGAQDRTYTMKEVLYFLQLQYIMTKRLYDEKQHQIVH 60	Db	17 SQIPASEQETLVRPKILLKLLKSGAQDRTYTMKEVLYFLQLQYIMTKRLYDEKQHQIVV 76
				Best Local Similarity 99.1%; Pred. No. 7e-64;	Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Qy	1 CSNDLIGDLFQVPSVKEHRKIVTMLYRNLYVNNQOBSSSDGTSVSEN 109	Db	17 CSNDLIGDLFQVPSVKEHRKIVTMLYRNLYVNNQOBSSSDGTSVSEN 125
				Best Local Similarity 99.1%; Pred. No. 7e-64;	Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Qy	1 CSNDLIGDLFQVPSVKEHRKIVTMLYRNLYVNNQOBSSSDGTSVSEN 109	Db	17 CSNDLIGDLFQVPSVKEHRKIVTMLYRNLYVNNQOBSSSDGTSVSEN 125

	RESULT	AA
17	SQTPASEEQTLVRKPLIKLKLKSVGAQDTYTMKEVLFVQITMTRKYDERQQHITYV	AA965567
61	CSDNLGGDIFGVPSFSVKERKTYTMIENLVVNOOESSDGETSVSEN	AA965567 standard: protein: 491 AA

..... DOCUMENT, PROCESS, ....  
XX  
AC AAY95567;  
.....

XX DT 12-SEP-2000 (first entry)  
XX  
RESULT 13

**AW94304** standard; protein; 491 AA.  
**AW94304** DEXX MDM2 oncoprotein.

AAW94304; KW  
retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;  
proliferation; immortal; tumour therapy; macular degeneration; activator;  
immuno; telomerase; catalytic; antioxidant; anti-oxidant; anti-oxidative;  
KW

13-APR-1999	(first entry)	KW XX	INK4 ; MDV2 ; oncoprotein.
Human	MDM2 :	QS	Homo sapiens.

Human; MDM2; p53; tumourigenesis; growth regulation; diagnosis;  
XX  
WO2000031238-A2.

Marginal fibrous histiocytoma; mRN; liposarcoma.  
Homo sapiens.  
02-JUN-2000.

PF 24-NOV-1993; 99WO-US022907.  
XX 25-NOV-1993; 9810S-0109991D  
PP US5858976-A.

EX 42 FEB-1999,  
PR 17-FEB-1999;  
XX 9905 0120549P.

07-APR-1992; 92US-00867840  
14-FEB-1991; 97US-00801718.  
(GENE-) GENETICA INC.  
PA XX  
PI Hannon GJ, Beach DH;

UR n-FOB; MM222222.  
XX  
PT New method for increasing the proliferative capacity of cell lines

Kinzler KW, Vogelstein B; PT comprises administering agents reversibly activating telomerase activity and reversibly inactivating Rb/INK4 and/or p53 pathways useful in treating age related diseases.

WPI; 1999-152105/13.  
N-PSDB; AAX03947.

XX  
Claim 5; Page 120; 123pp; English.  
PS  
PS

XX The invention concerns methods and reagents for extending the life-span,  
CC e.g. the number of mitotic divisions, of a cell. The method relies on  
CC

Claim 1; Col 23-28; 41pp; English.

The present invention describes: (1) a method for inhibiting the growth of tumour cells which contain a human MDM2 gene amplification, comprising

to human MDM2 (the present sequence); (2) a method as in (1) where the polypeptide lacks the homo-oligomerisation domain of p53; and (3) a polypeptide lacking the homologous domain of p53.

The method is useful for treating the following tumour types which have a MDM2 gene amplification: M-7 malignant fibrous histiocytoma (MFH), M-20 melanoma ab III (11) where the polypeptide lacks amino acids 130-333 of p53. The method is useful for treating the following tumour types which have a MDM2 gene amplification: M-7 malignant fibrous histiocytoma (MFH), M-20 melanoma ab III (11) where the polypeptide lacks amino acids 130-333 of p53.

the Rb and p16INK4a genes may also be used. The methods are useful for increasing the proliferative capacity of cells. The cells are subsequently of use in pharmaceutical and cosmetic preparations used to

Sequence 491 AA; treat conditions related to (premature) ageing, e.g. macular degeneration and arteriosclerosis. The cells can also be used to replace tumour cell

CC of growth and differentiation. Long lived (immortal) cells could also be  
CC used in the production of normal or genetically engineered  
CC biotechnology products

XX Sequence 491 AA:

Query Match 98.9%; Score 548; DB 3; Length 491;  
Best Local Similarity 99.1%; Pred. No. 7e-64;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 17 SQIPASEQETLVRPKPLKLUKSVGAQDFTYTMKEVLFLGQYIMTRLYDEKQHQIVY 76

Db 17 CSNDLIGD1RGVPSSVKEHRKITYMIXRNLYVNQESSSDSGTSEN 109

Db 77 CSNDLIGD1RGVPSSVKEHRKITYMIRNLVWVNQESSSDSGTSEN 125

Query Match 98.9%; Score 548; DB 3; Length 491;  
Best Local Similarity 99.1%; Pred. No. 7e-64;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 17 SQIPASEQETLVRPKPLKLUKSVGAQDFTYTMKEVLFLGQYIMTRLYDEKQHQIVY 60

Db 17 SQIPASEQETLVRPKPLKLUKSVGAQDFTYTMKEVLFLGQYIMTRLYDEKQHQIVY 76

Query Match 98.9%; Score 548; DB 3; Length 491;  
Best Local Similarity 99.1%; Pred. No. 7e-64;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 17 CSNDLIGD1RGVPSSVKEHRKITYMIXRNLYVNQESSSDSGTSEN 109

Db 77 CSNDLIGD1RGVPSSVKEHRKITYMIRNLVWVNQESSSDSGTSEN 125

RESULT 15

AAB48284 ID AAB48284 standard; protein; 491 AA.

XX AC AAB48284;

XX DT 02-APR-2001 (first entry)

XX DE Human MDM2 protein.

XX S-phase kinase associated protein; SKP1; SKP2;

KW SKP2-like protein; ZF; CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bak; Bad; Bcl-2; tumour; cytosolic.

XX OS Homo sapiens.

XX PN WO2000075184-A1.

XX PD 14-DEC-2000.

XX PF 05-JUN-2000; 2000WO-US015449.

XX PR 04-JUN-1999;

XX PA (UYYA ) UNIV YALE.

XX PI Zhang H, Tsvetkov LM, Kondo T;

XX DR WPI; 2001-061703/07.

XX N-PSDB; AAC84596.

XX PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,

PT involves altering levels of proteins such as S-phase kinase associated

XX proteins 1, 2 and cullin/CD53 proteins.

XX PS Claim 5; Page 93-95; 162pp; English.

XX The invention relates to methods of altering the polypeptide levels in a

CC cell, using proteins selected from S-phase kinase associated proteins 1

CC and 2 (SKP1, SKP2) SKP2-like proteins (ZF) and CUL-1 (a member of the

CC cullin/CD53 family of proteins). The method is useful for altering the

CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bak, Bad or Bcl-2

CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for

CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents

CC that modulate interactions between SKP and target proteins are useful for

CC treating tumours

XX Sequence 491 AA:

Query Match 98.9%; Score 548; DB 4; Length 491;

Best Local Similarity 99.1%; Pred. No. 7e-64;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

SQ 1 SQIPASEQETLVRPKPLKLUKSVGAQDFTYTMKEVLFLGQYIMTRLYDEKQHQIVY 60

Copyright GenCore version 5.1.6  
(c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2005, 08:21:09 ; Search time 43 Seconds  
(without alignments)  
185.227 Million cell updates/sec

Title: US-10-822-254-6  
Perfect score: 554  
Sequence: 1 SQIAPSEQETLVRPKPLIKK.....NLVVVNQESSDGGTYSSEN 109

Scoring table: BL03N62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:  
1: /cgn2\_6/pctodata/1/iaa/5A\_COMB.pep:  
2: /cgn2\_6/pctodata/1/iaa/5B\_COMB.pep:  
3: /cgn2\_6/pctodata/1/iaa/6A\_COMB.pep:  
4: /cgn2\_6/pctodata/1/iaa/6B\_COMB.pep:  
5: /cgn2\_6/pctodata/1/iaa/PCTUS\_COMB.pep:  
6: /cgn2\_6/pctodata/1/iaa/backfile1.pep:  
\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the core of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	98.9	188	4	US-09-603-052-4
2	548	98.9	491	1	US-07-303-103-2
3	548	98.9	491	1	US-08-044-619A-2
4	548	98.9	491	1	US-08-233-911-2
5	548	98.9	491	1	US-08-245-500A-3
6	548	98.9	491	1	US-08-390-546-3
7	548	98.9	491	1	US-08-330-472A-3
8	548	98.9	491	1	US-08-557-393-3
9	548	98.9	491	1	US-08-316C-3
10	548	98.9	491	1	US-08-330-517A-3
11	548	98.9	491	1	US-08-390-515A-3
12	548	98.9	491	2	US-08-801-718-3
13	548	98.9	491	3	US-09-170-152A-3
14	548	98.9	491	4	US-09-480-718-44
15	548	98.9	528	4	US-09-949-016-7125
16	548	98.9	528	4	US-09-949-016-7126
17	548	98.9	528	4	US-09-949-016-7127
18	548	98.9	528	4	US-09-949-016-7128
19	548	98.9	528	4	US-09-949-016-7129
20	531.5	95.9	216	3	US-09-510-252-4
21	488.5	88.2	489	1	US-07-903-103-4
22	488.5	88.2	489	1	US-08-044-612A-4
23	488.5	88.2	489	1	US-08-233-911-4
24	488.5	88.2	489	1	US-08-245-500A-5
25	488.5	88.2	489	1	US-08-316C-5
26	488.5	88.2	489	1	US-08-390-472A-5
27	488.5	88.2	489	1	US-08-557-393-5

ALIGMENTS

RESULT 1  
US-09-603-052-4  
; Sequence 4, Application US/09603052  
; Patent No. 6692116  
; GENERAL INFORMATION:  
; APPLICANT: Chene, Patrick  
; ADDRESS: Hochkeppel, Heinz-Kurt  
; TITLE OF INVENTION: Assay for identifying inhibitors of the interaction  
; FILE REFERENCE: MEWB26.001C1  
; CURRENT APPLICATION NUMBER: US/09-603-052  
; CURRENT FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: EP 95510576.9  
; PRIOR FILING DATE: 1995-09-18  
; PRIOR APPLICATION NUMBER: PCT/EP96/03957  
; PRIOR FILING DATE: 1996-09-10  
; NUMBER OF SEQ ID NOS: 11  
; SEQ ID NO 4  
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-603-052-4

Query Match 98 %; Score 548; DB 4;  
Best Local Similarity 99.1%; Pred. No. 5.4e-61;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASQETIVRPRBLILKLSVKAQRDTYTMKEVLFLYQYINTKRLYDEKQHIV 60  
Db 17 SQIPASQETIVRPRBLILKLSVKAQRDTYTMKEVLFLYQYINTKRLYDEKQHIV 76

Qy 61 CSNDLGDLFQYPSFSYKHKTYTMIRLYVNNQESSSDGTSYSEN 109  
Db 77 CSNDLGDLFQYPSFSYKHKTYTMIRLYVNNQESSSDGTSYSEN 125

RESULT 2  
US-07-903-103-2  
; Sequence 2, Application US/07903103  
; GENERAL INFORMATION:  
; APPLICANT: VOGELSTEIN, BERT  
; ADDRESS: KINZLER, KENNETH  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN HUMAN TUMORS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G ST., N.W.

CITY: WASHINGTON  
 STATE: D.C.  
 ZIP: 20001-4597  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 FILING DATE: 1992-06-23  
 APPLICANT NUMBER: US/07/903,103  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION NUMBER: US 07/867,840  
 FILING DATE: 07-APR-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KAGAN, SARAH A.  
 REGISTRATION NUMBER: 32,141  
 REFERENCE/DOCKET NUMBER: 01107.40148  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-508-9100  
 TELEFAX: 202-508-9299  
 TELEX: 197430 BBMB UT  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 491 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-903-103-2

Query Match 98.9%; Score 548; DB 1; Length 491;

Best Local Similarity 99.1%; Pred. No. 1.9e-50; Indels 0; Gaps 0;

Matches 108; Conservative 1; Mismatches 0; Gaps 0;  
 Qy 1 SQIPASEQETLVRPKPLKLLKSVGAQDVTMKEVLYFGVYIMTKRLYDEKQHIVH 60  
 Db 17 SQIPASEQETLVRPKPLKLLKSVGAQDVTMKEVLYFGVYIMTKRLYDEKQHIVY 76

Qy 61 CSNDLGLGFGYPSEFSVKEHRKLYTMVYRNLYVNQESSDSGTYSSEN 109  
 Db 77 CSNDLGLGFGYPSEFSVKEHRKLYTMVYRNLYVNQESSDSGTYSSEN 125

RESULT 3  
 US-08-044-619A-2

Sequence 2, Application US/08044619A

Patent No. 542063

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY

APPLICANT: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA

TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN

TITLE OF INVENTION: HUMAN TUMORS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT

STREET: 1001 G ST., N.W.

CITY: WASHINGTON

STATE: D.C.

ZIP: 20001-4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/044,619A

FILING DATE: 07-APR-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/903,103

RESULT 4  
 US-08-283-911-2

Sequence 2, Application US/08283911

Patent No. 551918

GENERAL INFORMATION:

APPLICANT: VOGELSTEIN, BERT

APPLICANT: KNIZLER, KENNETH

TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN

HUMAN TUMORS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: BANNER, BIRCH, MCKIE AND BECKETT

STREET: 1001 G ST., N.W.

CITY: WASHINGTON

STATE: D.C.

ZIP: 20001-4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/283,911

FILING DATE:

07-APR-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/903,103

FILING DATE: 07-APR-1992

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.40148

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

TELEX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 491 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-283-911-2

RESULT 5  
 US-08-245-500A-3  
 Sequence 3, Application US/08245500A  
 Patent No. 5550023  
 GENERAL INFORMATION:  
 APPLICANT: BURRELL, MARILLE  
 COMPUTER: HILL, DAVID E.  
 APPLICANT: KINZLER, KENNETH W.  
 COMPUTER: HILL, DAVID E.  
 APPLICANT: VOGELSTEIN, BERT  
 COMPUTER: HILL, DAVID E.  
 APPLICANT: VOGELSTEIN, BERT  
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 TITLE OF INVENTION: HUMAN TUMORS  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 STREET: 1001 G STREET, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20001  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/390,546  
 FILING DATE: 07-APR-1993  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KAGAN, SARAH A.  
 REGISTRATION NUMBER: 32,141  
 REFERENCE/DOCKET NUMBER: 01107-42798  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-508-9000  
 TELEFAX: 202-508-9299  
 TELEX: 197430 BBMB UT  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 491 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-390-546-3

Query Match 98.9%; Score 548; DB 1; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 1.9e-60;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLKLSVGAQDVTYTMKEVLFLYQYIMTRLYDEKQHIVH 60  
 Db 17 SQIPASEQETLVRPKPLLKLSVGAQDVTYTMKEVLFLYQYIMTRLYDEKQHIVY 76

Qy 61 CSNDLIGDLFGYPSPFSVKEHRKITYMIRNLVNNQQESSSDSGTSVSEN 109  
 Db 77 CSNDLIGDLFGYPSPFSVKEHRKITYMIRNLVNNQQESSSDSGTSVSEN 125

RESULT 6  
 US-08-390-546-3  
 Sequence 3, Application US/08390546  
 Patent No. 5606044  
 GENERAL INFORMATION:  
 APPLICANT: BURRELL, MARILLE  
 COMPUTER: HILL, DAVID E.  
 APPLICANT: KINZLER, KENNETH W.  
 COMPUTER: HILL, DAVID E.  
 APPLICANT: VOGELSTEIN, BERT  
 COMPUTER: HILL, DAVID E.  
 APPLICANT: VOGELSTEIN, BERT  
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 TITLE OF INVENTION: HUMAN TUMORS  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 STREET: 1001 G STREET, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20001  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/390,546  
 FILING DATE: 07-APR-1993  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KAGAN, SARAH A.  
 REGISTRATION NUMBER: 32,141  
 REFERENCE/DOCKET NUMBER: 01107-42798  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-508-9000  
 TELEFAX: 202-508-9299  
 TELEX: 197430 BBMB UT  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 491 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-390-546-3

Query Match 98.9%; Score 548; DB 1; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 1.9e-60;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLKLSVGAQDVTYTMKEVLFLYQYIMTRLYDEKQHIVH 60  
 Db 17 SQIPASEQETLVRPKPLLKLSVGAQDVTYTMKEVLFLYQYIMTRLYDEKQHIVY 76

Qy 61 CSNDLIGDLFGYPSPFSVKEHRKITYMIRNLVNNQQESSSDSGTSVSEN 109  
 Db 77 CSNDLIGDLFGYPSPFSVKEHRKITYMIRNLVNNQQESSSDSGTSVSEN 125

RESULT 7  
 US-08-390-479A-3  
 Sequence 3, Application US/08390479A  
 Patent No. 5618921  
 GENERAL INFORMATION:  
 APPLICANT: BURRELL, MARILLE  
 COMPUTER: HILL, DAVID E.  
 APPLICANT: KINZLER, KENNETH W.  
 COMPUTER: HILL, DAVID E.  
 APPLICANT: VOGELSTEIN, BERT  
 COMPUTER: HILL, DAVID E.  
 APPLICANT: VOGELSTEIN, BERT  
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 TITLE OF INVENTION: HUMAN TUMORS  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & WITCOFF, LTD.  
STREET: 1001 G STREET, N.W.  
STATE: D.C.  
ZIP: 20001  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,479A  
FILING DATE: 02-FEB-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.48992  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BMB UT  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-390-479A-3

## Query Match 98.9%; Score 548; DB 1; Length 491;

Best Local Similarity 99.1%; Pred. No. 1.9e-60; Indels 0; Gaps 0;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Sequence 3, Application US/08557393  
Patent No. 5702903  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
TITLE OF INVENTION: HUMAN TUMORS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,516C  
FILING DATE: 07-APR-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BMB UT  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-390-516C-3

## Query Match 98.9%; Score 548; DB 1; Length 491;

Best Local Similarity 99.1%; Pred. No. 1.9e-60; Indels 0; Gaps 0;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Sequence 3, Application US/08390516C  
Patent No. 5708116  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
TITLE OF INVENTION: HUMAN TUMORS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,516C  
FILING DATE: 07-APR-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798

Query Match 98.9%; Score 548; DB 1; Length 491;  
Best Local Similarity 99.1%; Pred. No. 1.9e-60; Indels 0; Gaps 0;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Sequence 1, Application US/08390516C  
Patent No. 5708116  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
TITLE OF INVENTION: HUMAN TUMORS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/557,393  
FILING DATE: 13-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

Query Match 98.9%; Score 548; DB 1; Length 491;  
Best Local Similarity 99.1%; Pred. No. 1.9e-60; Indels 0; Gaps 0;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Sequence 1, Application US/08390516C  
Patent No. 5708116  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
TITLE OF INVENTION: HUMAN TUMORS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/557,393  
FILING DATE: 13-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

US-08-390-516C-3

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 Best Local Similarity 99.1%; Pred. No. 1.9e-60;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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 Db 17 SQIPASEQETLVRPKPLKLKLSVGAQDVTMKEVLFLYQYIMTRLYDEKQHIVY 76

Qy 61 CSNDLIGDLFGVPSFSYKEHRKITYMVRNLVVNQESSSDSGTSVSEN 109  
 Db 77 CSNDLIGDLFGVPSFSYKEHRKITYMVRNLVVNQESSSDSGTSVSEN 125

RESULT 10

US-08-390-517A-3  
 Sequence 3, Application US/08390517A  
 Patent No. 5736338

GENERAL INFORMATION:  
 APPLICANT: BURRELL, MARILEE  
 APPLICANT: HILL, DAVID E.  
 APPLICANT: KINZLER, KENNETH W.  
 APPLICANT: VOGELSTEIN, BERT  
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 NUMBER OF SEQUENCES: 9  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 STREET: 1001 G STREET, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 ZIP: 20001

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/390, 515A  
 FILING DATE: 07-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KAGAN, SARAH A.  
 REGISTRATION NUMBER: 32,141  
 REFERENCE/DOCKET NUMBER: 01107.42798  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-508-9100  
 TELEX: 197430 BBMB UT  
 INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 491 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-390-515A-3

Query Match 98.9%; Score 548; DB 1; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 1.9e-60;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLKLKLSVGAQDVTMKEVLFLYQYIMTRLYDEKQHIVH 60  
 Db 17 SQIPASEQETLVRPKPLKLKLSVGAQDVTMKEVLFLYQYIMTRLYDEKQHIVY 76

Qy 61 CSNDLIGDLFGVPSFSYKEHRKITYMVRNLVVNQESSSDSGTSVSEN 109  
 Db 77 CSNDLIGDLFGVPSFSYKEHRKITYMVRNLVVNQESSSDSGTSVSEN 125

RESULT 12

US-08-390-517A-3  
 Sequence 3, Application US/08390517A  
 Patent No. 5736338

GENERAL INFORMATION:  
 APPLICANT: BURRELL, MARILEE  
 APPLICANT: HILL, DAVID E.  
 APPLICANT: KINZLER, KENNETH W.  
 APPLICANT: VOGELSTEIN, BERT  
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 NUMBER OF SEQUENCES: 9  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 STREET: 1001 G STREET, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.

RESULT 11

COUNTRY: USA  
 ZIP: 20001  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/801,718  
 FILING DATE: 14-FEB-1997.  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/390,515  
 FILING DATE: 07-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KAGAN, SARAH A.  
 REFERENCE/DOCKET NUMBER: 32,141  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (02) 508-9100  
 TELEX: 197430 BMB UT  
 TELEX: 202508-9239  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 491 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 S-08-801-718\_3

Query Match Score 548; DB 2; Le  
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 Matches 108; Conservative 1; Mismatches 0;

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b	17	SQIPASEQETIVPKPLI.KKLLKSVGAQKDYYTMKEYLVFY
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b	77	CSDNLGDFGVPSFVKEHRKLYTMIVRNLYVNQQESSI

RESULT 13  
 S-09-170-159A-3  
 Sequence 3, Application US/09170159A  
 Patent No. 6399755  
 GENERAL INFORMATION:  
 APPLICANT: BURKELL, MARILIE  
 HILL, DAVID E.  
 KIMZLER, KENNETH W.  
 VOGELSTEIN, BERT  
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDI  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BANNER, BIRCH, MCKIE AND BECK  
 STREET: 1001 G STREET, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20001  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version  
 CURRENT APPLICATION DATA: US/09/170,159A  
 APPLICATION NUMBER: US/09/170,159A  
 FILING DATE: 13-Oct-1998  
 CLASSIFIER: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KAGAN, SARAH A.

```

REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107-42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-5299
TELEX: 197430 BMB UT

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-170-159A-3

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Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; C
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Qy      61 CSNDLGLDFGVPSFSVKERHKIYTMYRNLYVNQEQESSSDGTSSEN 109
Db      77 CSNDLGLDFGVPSFSVKERHKIYTMYRNLYVNQEQESSSDGTSSEN 125

RESULT 14
US-09-480-718-44
Sequence 44, Application US/09480718
Patent No. 6407662
GENERAL INFORMATION:
APPLICANT: Sherr, Charles J
APPLICANT: Weber, Jason D.
APPLICANT: Rousell, Martine F.
APPLICANT: Frederique, Zindy
TITLE OF INVENTION: ARF-19, A NOVEL REGULATOR OF THE MAMMALIAN CELL
FILE REFERENCE: 1340-1-0-3 CIP 1
CURRENT APPLICATION NUMBER: US/09/480,718
CURRENT FILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: 09/129,855
EARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44
LENGTH: 491
TYPE: PRT
ORGANISM: Homo sapiens
US-09-480-718-44

Query Match      98.9%; Score 548; DB 4; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; C
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Db      17 SQIPASEQETLVRPKPLILKLSVGAQKDITTMKEVLFYLGQYIMTKRLYDEKQO
Qy      61 CSNDLGLDFGVPSFSVKERHKIYTMYRNLYVNQEQESSSDGTSSEN 109
Db      77 CSNDLGLDFGVPSFSVKERHKIYTMYRNLYVNQEQESSSDGTSSEN 125

RESULT 15
US-09-949-016-7125
Sequence 7125, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENNER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND

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FILE REFERENCE: CL001307
| CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14
| PRIOR FILING DATE: 2000-10-20
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR FILING DATE: 2000-10-03
| PRIOR APPLICATION NUMBER: 60/237,768
| PRIOR FILING DATE: 2000-09-08
| PRIOR APPLICATION NUMBER: 60/231,498
| NUMBER OF SEQ ID NOS: 207012
| SOFTWARE: Fast-SEQ for Windows Version 4.0
| SEQ ID NO: 7125
| LENGTH: 528
| TYPE: PRT
| ORGANISM: Human
US-09-949-016-7125

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Matches 108;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;
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(c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

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Scoring table: BLOSUM62

Title: US-10-822-254-6

Perfect score: 554

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Query Score	Match Score	Length	DB ID	Description
1	548	98.9	491	9 US-09-888-077-1	Sequence 1, Appli
2	548	98.9	491	9 US-09-956-425-8	Sequence 8, Appli
3	548	98.9	491	10 US-09-029-327-2	Sequence 2, Appli
4	548	98.9	491	11 US-09-16724-2	Sequence 7, Appli
5	548	98.9	491	15 US-10-422-336-137	Sequence 137, Appli
6	548	98.9	491	15 US-10-232-951-35	Sequence 35, Appli
7	548	98.9	491	16 US-10-885-838-1	Sequence 1, Appli
8	531.5	95.9	216	13 US-10-057-510-4	Sequence 4, Appli
9	522.5	94.3	522	15 US-10-287-326-380	Sequence 380, App
10	488.5	94.3	522	15 US-10-587-326-382	Sequence 382, App
11	488.5	88.2	489	9 US-09-956-425-6	Sequence 6, Appli
12	488.5	88.2	489	11 US-09-966-724-4	Sequence 4, Appli
13	481	86.8	95	16 US-10-685-838-2	Sequence 2, Appli

**SEQUENCES**

Sequence 4, Appli  
Sequence 3, Appli  
Sequence 143, App  
Sequence 17237, Sequence 3, Appli  
Sequence 5071, Ap  
Sequence 11326, Sequence 59020, A  
Sequence 16555, A  
Sequence 45311, A  
Sequence 236213, Sequence 54, App1  
Sequence 63455, A  
Sequence 2452, Ap  
Sequence 7409, Ap  
Sequence 282-122A-545311  
Sequence 257589, Sequence 6345, A  
Sequence 382, App  
Sequence 172, App  
Sequence 7410, Ap  
Sequence 2, Appli  
Sequence 257589, Sequence 59572, A  
Sequence 169953, Sequence 7027, Ap  
Sequence 61364, A  
Sequence 818, App  
Sequence 133574, Sequence 819, App  
Sequence 2420, Ap

**ALIGNMENTS**

RESULT 1 US-09-888-077-1 ; Sequence 1, Application US-09888077 ; Patient No. US2003031818A1 ; GENERAL INFORMATION ; APPLICANT: Ronai, Ze, ev ; Fuchs, Serge ; TITLE OF INVENTION: Modification of Mdm2 Activity ; FILE REFERENCE: 24201H19-US1 ; CURRENT APPLICATION NUMBER: US-09-888-077 ; CURRENT FILING DATE: 2003-06-22 ; PRIOR APPLICATION NUMBER: US-60/213,343 ; PRIORITY FILING DATE: 2000-06-22 ; NUMBER OF SEQ ID NOS: 3 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 1 ; LENGTH: 491 ; TYPE: PRT ; ORGANISM: Homo sapiens ; US-09-888-077-1

Query Match 98.9%; Score 548; DB 9; Length 491;  
Best Local Similarity 99.1%; Pred. No. 2.8e-56;  
Matches 108; Conservate 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLIKLKSKGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60  
Db 17 SQIPASEQETLVRPKPLIKLKSKGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVV 76

Qy 61 CSNDLIGDLFQVPSFSVKERKITYMIVRNLYWVHQESSDSGTYSSEN 109  
Db 77 CSNDLIGDLFQVPSFSVKERKITYMIVRNLYWVHQESSDSGTYSSEN 125

RESULT 2 US-09-956-425-8

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Sequence 8, Application US/0956425
Patent No. US2002004519A1

GENERAL INFORMATION:
APPLICANT: Kriwacki, Richard
APPLICANT: Bothner, Brian
APPLICANT: Lewis, William
TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
FILE REFERENCE: 134 0/1/035
CURRENT APPLICATION NUMBER: US/09/956,425
CURRENT FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 8
LENGTH: 491
TYPE: PRT
ORGANISM: Homo sapiens
US-09-956-425-8

Query Match: 98.9%; Score 548; DB 9; Length 491;
Best Local Similarity 99.1%; Pred. No. 2.8e-0; Indels 0; Gaps 0;
Matches 108; Conservative 1; Mismatches 0;

Qy 1 SQIPASEQETLVRPKPLIKLKSVGQKDTYTMKEVLFYLQYIMTKRLYBKKQHQIVH 60
Db 17 SQIPASEQETLVRPKPLIKLKSVGQKDTYTMKEVLFYLQYIMTKRLYBKKQHQIVH 76

Qy 61 CSNDLIGLDLGPGPSFSKVHRKXITYMTRNLVVVNQQESSDGTGSVSEN 109
Db 77 CSNDLIGLDLGPGPSFSKVHRKXITYMTRNLVVVNQQESSDGTGSVSEN 125

RESULT 3
US-09-029-327-2
Sequence 2, Application US/09029327
Publication No. US20030060432A1
GENERAL INFORMATION:
APPLICANT: TOCQUE, Bruno
APPLICANT: WASILYK, Bohdan
APPLICANT: DUBS-POERSZMAN,
APPLICANT: Marie-Christine
TITLE OF INVENTION: ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
TITLE OF INVENTION: THE PROTEIN MNM2, AND USE THEREOF IN THE TREATMENT OF
TITLE OF INVENTION: CANCERS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
ZIP: 19426
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/029,327
FILING DATE:
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: FR 96/01340
FILING DATE: 02-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR95/10331
FILING DATE: 04-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fehliner EBG., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: ST95050-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-2800

```

```

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein

JS-09-029-327-2

RESULT 4
US-09-966-724-2
Sequence 2, Application US/09966724
Publication No. US20040170971A1

GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY
720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
HUMAN TUMORS

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G ST., N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/966,724
FILING DATE: 01-Oct-2001
CLASIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/044,619
FILING DATE: 2001-10-01
APPLICATION NUMBER: US 07/867,840
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.40148

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197410 BRW UT

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match          98.9%; Score 548; DB 11; Length 491;
Best Local Similarity 99.1%; Pred. No. 2.8e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match          98.9%; Score 548; DB 11; Length 491;
Best Local Similarity 99.1%; Pred. No. 2.8e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy                   1 SQIPASQETLVRPKPILLKILKSQGAQDVTYTMKEVLFLVQYIMTRLYDEKQHQIVY 60
Db                   17 SQIPASQETLVRPKPILLKILKSQGAQDVTYTMKEVLFLVQYIMTRLYDEKQHQIVY 76
Qy                   61 CSNDLGLDFGVPFSVKEHRKIYTMVYRLNLVNNQQESSSDSGTSVSEN 109
Db                   77 CSNDLGLDFGVPFSVKEHRKIYTMVYRLNLVNNQQESSSDSGTSVSEN 125

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Qy 1 SQIPASEQETLVRPKPLKLKSVGAQKDITYTMKEVLFYLQYIMTKRLYDEKOHHIVH 60  
 Db 17 SQIPASEQETLVRPKPLKLKSVGAQKDITYTMKEVLFYLQYIMTKRLYDEKOHHIVV 76

Qy 61 CSNDLGLFGVPFSVYERKRYTMYRNLYVNQESSSDSGTSVSEN 109  
 Db 77 CSNDLGLFGVPFSVYERKRYTMYRNLYVNQESSSDSGTSVSEN 125

**RESULT 5**  
 US-10-422-536-137  
 Sequence 137, Application US/10422536  
 Publication No. -US2004001400A1  
 GENERAL INFORMATION:  
 APPLICANT: Kinsella, Todd  
 APPLICANT: Lorenz, James  
 APPLICANT: Pray, Todd  
 APPLICANT: Bennett, Mark  
 TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR INHIBITING  
 FILE REFERENCE: A-71431-1/AMP/CYO  
 CURRENT APPLICATION NUMBER: US/10/422,536  
 CURRENT FILING DATE: 2003-04-23  
 PRIOR APPLICATION NUMBER: US 60/187,130  
 PRIOR FILING DATE: 2000-03-06  
 PRIOR APPLICATION NUMBER: US 09/800,770  
 PRIOR FILING DATE: 2001-03-06  
 PRIOR APPLICATION NUMBER: US 10/232,758  
 PRIOR FILING DATE: 2002-08-30  
 NUMBER OF SEQ ID NOS: 168  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 137  
 LENGTH: 491  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-422-536-137

Query Match 98.9%; Score 548; DB 15; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 2.8e-56;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLKLKSVGAQKDITYTMKEVLFYLQYIMTKRLYDEKOHHIVH 60  
 Db 17 SQIPASEQETLVRPKPLKLKSVGAQKDITYTMKEVLFYLQYIMTKRLYDEKOHHIVV 76

Qy 61 CSNDLGLFGVPFSVYERKRYTMYRNLYVNQESSSDSGTSVSEN 109  
 Db 77 CSNDLGLFGVPFSVYERKRYTMYRNLYVNQESSSDSGTSVSEN 125

**RESULT 6**  
 US-10-232-051-35  
 Sequence 35, Application US/10232951  
 Publication No. -US20040043386A1  
 GENERAL INFORMATION:  
 APPLICANT: Pray, Todd  
 APPLICANT: Wong, Brian  
 APPLICANT: Bennett, Mark  
 APPLICANT: Parlati, Francesco  
 APPLICANT: Rigel Pharmaceuticals, Incorporated  
 TITLE OF INVENTION: Methods and Compositions for Functional Ubiquitin  
 FILE REFERENCE: 021044-006800US  
 CURRENT APPLICATION NUMBER: US/10/232,951  
 CURRENT FILING DATE: 2002-08-30  
 NUMBER OF SEQ ID NOS: 35  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 35  
 LENGTH: 491  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE: E3 ubiquitin ligating agent mouse double minute 2

OTHER INFORMATION: (mdm2) homolog full length protein isoform, mouse  
 OTHER INFORMATION: P53-binding protein (MDM2) homolog, transcript  
 OTHER INFORMATION: variant MDM2, transformed 3T3 cell, double minute 2,  
 OTHER INFORMATION: Mdm2 cDNA  
 US-10-232-951-35

Query Match 98.9%; Score 548; DB 15; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 2.8e-56;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLKLKSVGAQKDITYTMKEVLFYLQYIMTKRLYDEKOHHIVH 60  
 Db 17 SQIPASEQETLVRPKPLKLKSVGAQKDITYTMKEVLFYLQYIMTKRLYDEKOHHIVV 76

Qy 61 CSNDLGLFGVPFSVYERKRYTMYRNLYVNQESSSDSGTSVSEN 109  
 Db 77 CSNDLGLFGVPFSVYERKRYTMYRNLYVNQESSSDSGTSVSEN 125

**RESULT 7**  
 US-10-685-838-1  
 Sequence 1, Application US/10685838  
 Publication No. US20040197893A1  
 GENERAL INFORMATION:  
 APPLICANT: SHUBERT, CARSTEN  
 APPLICANT: GRASBERGER, BRUCE  
 APPLICANT: MAGUIRE, DIANE  
 APPLICANT: DECRAN, INGRID  
 APPLICANT: SPURILINO, JOHN  
 TITLE OF INVENTION: HDM2 -INHIBITOR COMPLEXES AND USES THEREOF  
 FILE REFERENCE: PRD-2137-USNP  
 CURRENT APPLICATION NUMBER: US/10/685,838  
 CURRENT FILING DATE: 2003-10-15  
 PRIORITY: 2002-10-16  
 PRIORITY APPLICATION NUMBER: 60/418,350  
 PRIORITY FILING DATE: 2002-10-16  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 3.2  
 SEQ ID NO: 1  
 PRIORITY: 2003-10-15  
 PRIORITY FILING DATE: 2002-10-16  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 3.2  
 SEQ ID NO: 1  
 ORGANISM: Homo sapiens  
 US-10-685-838-1

Query Match 98.9%; Score 548; DB 15; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 2.8e-56;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLKLKSVGAQKDITYTMKEVLFYLQYIMTKRLYDEKOHHIVH 60  
 Db 17 SQIPASEQETLVRPKPLKLKSVGAQKDITYTMKEVLFYLQYIMTKRLYDEKOHHIVV 76

Qy 61 CSNDLGLFGVPFSVYERKRYTMYRNLYVNQESSSDSGTSVSEN 109  
 Db 77 CSNDLGLFGVPFSVYERKRYTMYRNLYVNQESSSDSGTSVSEN 125

**RESULT 8**  
 US-10-057-510-4  
 Sequence 4, Application US/10057510  
 Publication No. US20020098580A1  
 GENERAL INFORMATION:  
 APPLICANT: Nandabalan, Krishnan  
 APPLICANT: Yang, Meijia  
 APPLICANT: Schulz, Vincent  
 APPLICANT: Curaden Corporation  
 TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF  
 FILE REFERENCE: 15966-524 MDM US  
 CURRENT APPLICATION NUMBER: US/10/057,510  
 CURRENT FILING DATE: 2002-01-25  
 PRIORITY: 2000-02-22  
 PRIORITY APPLICATION NUMBER: US/09/510,252  
 PRIORITY FILING DATE: 2000-02-22  
 PRIORITY APPLICATION NUMBER: US/09/510,252  
 PRIORITY FILING DATE: 1999-02-23

PRIOR APPLICATION NUMBER: USN 60/122,643  
 / PRIOR FILING DATE: 1999-03-03  
 / NUMBER OF SEQ ID NOS: 4  
 / SOFTWARE: PatentIn Ver. 2.0  
 / SEQ ID NO: 4  
 / LENGTH: 216  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 US-10-057-510-4

Query Match 95.9%; Score 531.5; DB 13; Length 216;  
 Best Local Similarity 98.2%; Pred. No. 8.7e-55; Mismatches 1; Indels 1; Gaps 1;  
 Matches 107; Conservative 1; Mismatches 0; Indels 0; Gaps 1;

Qy 1 SQIPASEQETLVRPKPLKLLKLSVQAQDVTYTMKEVLFTLGOYIMTKRLYDEKQHIVH 60  
 Db 17 SQIPASEQETLVRPKPLKLLKLSVQAQDVTYTMKEVLFTLGOYIMTKRLYDEKQHIVY 75

Qy 61 CSNDLIGDLFQGVPSFSTVKERHKIYTMVNLVVVNQESSSDSGTYSSEN 109  
 Db 76 CSNDLIGDLFQGVPSFSTVKERHKIYTMVNLVVVNQESSSDSGTYSSEN 124

RESULT 9  
 US-10-287-226-380  
 / Sequence 380, Application US/10287226  
 / Publication No. US200401086875A1

/ GENERAL INFORMATION:  
 / APPLICANT: Agee, Michele L.,  
 / APPLICANT: Alsobrook, John P.,  
 / APPLICANT: Berghs, Constance,  
 / APPLICANT: Boldog, Ference,  
 / APPLICANT: Burgess, Catherine E.,  
 / APPLICANT: Chant, John S.,  
 / APPLICANT: Chaudhuri, Amitabha,  
 / APPLICANT: DiPippo, Vincent A.,  
 / APPLICANT: Edinger, Shlomit R.,  
 / APPLICANT: Eisen, Andrew,  
 / APPLICANT: Ellerman, Karen,  
 / APPLICANT: Gorman, Linda,  
 / APPLICANT: Gerlach, Valerie,  
 / APPLICANT: Ji, Weizhen,  
 / APPLICANT: Kekuda, Ramesh,  
 / APPLICANT: Khrantsov, Nikolai,  
 / APPLICANT: Li, Li,  
 / APPLICANT: Malynkar, Uriel M.,  
 / APPLICANT: MacDougal, John R.,  
 / APPLICANT: Mezes, Peter S.,  
 / APPLICANT: Miller, Charles E.,  
 / APPLICANT: Millet, Isabelle,  
 / APPLICANT: Ooi, Chean Eng,  
 / APPLICANT: Ort, Tatiana,  
 / APPLICANT: Padigaru, Muralidhara,  
 / APPLICANT: Paturajan, Meera,  
 / APPLICANT: Rastelli, Luca,  
 / APPLICANT: Rieger, Daniel K.,  
 / APPLICANT: Rothenberg, Mark E.,  
 / APPLICANT: Shenoy, Suresh G.,  
 / APPLICANT: Spadera, Steven K.,  
 / APPLICANT: Spytek, Kimberly A.,  
 / APPLICANT: Taupier, Jr., Raymond J.,  
 / APPLICANT: Vernet, Corine A.M.,  
 / APPLICANT: Zerhusen, Bryan D.,  
 / APPLICANT: Zhong, Mei

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
 FILE REFERENCE: 21A102-40C  
 CURRENT APPLICATION NUMBER: US/10/287-226  
 CURRENT FILING DATE: 2002-11-04  
 PRIOR APPLICATION NUMBER: 60/334,421  
 PRIOR FILING DATE: 2001-11-30  
 PRIOR APPLICATION NUMBER: 60/354,392  
 PRIOR FILING DATE: 2002-02-04

PRIOR APPLICATION NUMBER: 60/360,148  
 / PRIOR FILING DATE: 2002-02-27  
 / PRIOR APPLICATION NUMBER: 60/364,000  
 / PRIOR FILING DATE: 2002-03-13  
 / PRIOR APPLICATION NUMBER: 60/404,821  
 / PRIOR FILING DATE: 2002-05-20  
 / PRIOR APPLICATION NUMBER: 60/334,526  
 / PRIOR FILING DATE: 2001-11-30  
 / PRIOR APPLICATION NUMBER: 60/354,409  
 / PRIOR FILING DATE: 2002-07-04  
 / PRIOR APPLICATION NUMBER: 60/364,227  
 / PRIOR FILING DATE: 2002-07-13  
 / PRIOR APPLICATION NUMBER: 60/334,027  
 / PRIOR FILING DATE: 2001-11-28  
 / PRIOR APPLICATION NUMBER: 60/331,641  
 / PRIOR FILING DATE: 2001-11-20  
 / Remaining Prior Application data removed - See File Wrapper or PALM.  
 / NUMBER OF SEQ ID NOS: 673  
 / SOFTWARE: CurassEqList version 0.1  
 / SEQ ID NO: 380  
 / LENGTH: 522  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 US-10-287-226-380

Query Match 94.3%; Score 522.5; DB 15; Length 522;  
 Best Local Similarity 77.1%; Pred. No. 3.3e-53; Mismatches 1; Indels 0; Gaps 31; Gaps 1;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 31; Gaps 1;

Qy 1 SQIPASEQETLVRPKPLKLLKLSVQAQDVTYTMKE-----36  
 Db 17 SQIPASEQETLVRPKPLKLLKLSVQAQDVTYTMKEWSFTMLPRLVNNSWAQGICLPRP 76

Qy 37 -----VLPYLQQTIMTRLYDEKQHIVYCSNDLGLGDFGVPFPSVKERHKIYTMVYR 89  
 Db 77 PKVLDLQVLFLQQTIMTRLYDEKQHIVYCSNDLGLGDFGVPSFSVKERHKIYTMVYR 136

Qy 90 NLVYNQQESSSDSGTYSSEN 109  
 Db 137 NLVYNQQESSSDSGTYSSEN 156

RESULT 10  
 US-10-287-226-382  
 / Sequence 382, Application US/10287226  
 / Publication No. US200401086875A1

/ GENERAL INFORMATION:  
 / APPLICANT: Agee, Michele L.,  
 / APPLICANT: Alsobrook, John P.,  
 / APPLICANT: Berghs, Constance,  
 / APPLICANT: Boldog, Ference,  
 / APPLICANT: Burgess, Catherine E.,  
 / APPLICANT: Chant, John S.,  
 / APPLICANT: Chaudhuri, Amitabha,  
 / APPLICANT: DiPippo, Vincent A.,  
 / APPLICANT: Edinger, Shlomit R.,  
 / APPLICANT: Eisen, Andrew,  
 / APPLICANT: Ellerman, Karen,  
 / APPLICANT: Gorman, Linda,  
 / APPLICANT: Gerlach, Valerie,  
 / APPLICANT: Ji, Weizhen,  
 / APPLICANT: Kekuda, Ramesh,  
 / APPLICANT: Khrantsov, Nikolai,  
 / APPLICANT: Li, Li,  
 / APPLICANT: Malynkar, Uriel M.,  
 / APPLICANT: MacDougal, John R.,  
 / APPLICANT: Mezes, Peter S.,  
 / APPLICANT: Miller, Charles E.,  
 / APPLICANT: Millet, Isabelle,  
 / APPLICANT: Ooi, Chean Eng,  
 / APPLICANT: Ort, Tatiana,  
 / APPLICANT: Padigaru, Muralidhara,  
 / APPLICANT: Paturajan, Meera,  
 / APPLICANT: Rastelli, Luca,  
 / APPLICANT: Rieger, Daniel K.,  
 / APPLICANT: Rothenberg, Mark E.,  
 / APPLICANT: Shenoy, Suresh G.,  
 / APPLICANT: Spadera, Steven K.,  
 / APPLICANT: Spytek, Kimberly A.,  
 / APPLICANT: Taupier, Jr., Raymond J.,  
 / APPLICANT: Vernet, Corine A.M.,  
 / APPLICANT: Zerhusen, Bryan D.,  
 / APPLICANT: Zhong, Mei

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
 CURRENT APPLICATION NUMBER: US/10/287-226  
 CURRENT FILING DATE: 2002-11-04  
 PRIOR APPLICATION NUMBER: 60/334,421  
 PRIOR FILING DATE: 2001-11-30  
 PRIOR APPLICATION NUMBER: 60/354,392  
 PRIOR FILING DATE: 2002-02-04

/ APPLICANT: Li, Li,  
 / APPLICANT: Malvankar, Uriel M.,  
 / APPLICANT: MacDougal, John R.,  
 / APPLICANT: Mezes, Peter S.,  
 / APPLICANT: Miller, Charles E.,  
 / APPLICANT: Millet, Isabelle,  
 / APPLICANT: Ooi, Chean Eng,  
 / APPLICANT: Ort, Tatiana,  
 / APPLICANT: Padigaru, Muralidhara,

APPLICANT: Paturajan, Meera,  
 APPLICANT: Rastelli, Luca,  
 APPLICANT: Rieger, Daniel K.,  
 APPLICANT: Rothenberg, Mark E.,  
 APPLICANT: Shenoy, Suresh G.,  
 APPLICANT: Spadera, Steven K.,  
 APPLICANT: Spytek, Kimberley A.,  
 APPLICANT: Taupier, Jr., Raymond J.,  
 APPLICANT: Vernet, Corine A.M.,  
 APPLICANT: Zarhouni, Bryan D.,  
 APPLICANT: Zhong, Mei

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: 2:14:02-180C

CURRENT APPLICATION NUMBER: US/10/287,226

CURRENT FILING DATE: 2002-11-04

PRIOR APPLICATION NUMBER: 6/0/334,421

PRIOR FILING DATE: 2001-11-30

PRIOR APPLICATION NUMBER: 6/0/354,392

PRIOR FILING DATE: 2002-02-04

PRIOR APPLICATION NUMBER: 6/0/360,148

PRIOR FILING DATE: 2002-02-27

PRIOR APPLICATION NUMBER: 6/0/364,000

PRIOR FILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: 6/0/404,821

PRIOR FILING DATE: 2002-08-20

PRIOR APPLICATION NUMBER: 6/0/334,526

PRIOR FILING DATE: 2001-11-30

PRIOR APPLICATION NUMBER: 6/0/354,409

PRIOR FILING DATE: 2002-02-04

PRIOR APPLICATION NUMBER: 6/0/364,227

PRIOR FILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: 6/0/334,027

PRIOR FILING DATE: 2001-11-28

PRIOR APPLICATION NUMBER: 6/0/331,641

PRIOR FILING DATE: 2001-11-20

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 673

SOFTWARE: CuraSeqist version 0.1

SEQ ID NO: 382

LENGTH: 522

TYPE: PRT

ORGANISM: Homo sapiens

US-10-287-226-382

Query Match 94.3%; Score 522.5; DB 15; Length 522;  
 Best Local Similarity 77.1%; Pred. No. 3.3e-53;  
 Matches 108; Conservative 1; Mismatches 0; Indels 31; Gaps 1;

Qy 1 SQIPASBOETLVRPKPLLKLUKSVGAQDVTYTMKE-----36  
 Db 17 SQIPASEQETLVRPKPLLKLUKSVGAQDVTYTMKEWSFTMLPRLVWNSWAQGICLPRP 76

Qy 37 -----VLFYLGQXIMTKRILDEKOOHIVCSNDLIGDLFGVPSFSVKEHRKITYTMIYR 89  
 Db 77 PRVLDLQWLFYLGQYIMTKRILDEKOOHIVCSNDLIGDLFGVPSFSVKEHRKITYTMIYR 136

Qy 90 NLVYVVNQESSDSGTYSSEN 109  
 Db 137 NLVYVVNQESSDSGTYSSEN 156

RESULT 11  
 US-09-956-425-6

Sequence 6, Application US/09956425  
 Patent No. US20020045192A1  
 GENERAL INFORMATION:  
 APPLICANT: Kriwacki, Richard  
 APPLICANT: Bothner, Brian  
 APPLICANT: Lewis, William  
 TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof  
 FILE REFERENCE: 1340/1/035  
 CURRENT APPLICATION NUMBER: US/09/956,425  
 CURRENT FILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 25  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 6  
 LENGTH: 489  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-09-956-425-6

Query Match 88.2%; Score 488.5; DB 9; Length 489;  
 Best Local Similarity 87.2%; Pred. No. 3.3e-49;  
 Matches 95; Conservative 8; Mismatches 3; Indels 3; Gaps 1;

Qy 1 SQIPASBOETLVRPKPLLKLUKSVGAQDVTYTMKEBVLPFLQYIMTKRILDEKOOHIV 60  
 Db 17 SQIPASEQETLVRPKPLLKLUKSVGAQDVTYTMKEBVLPFLQYIMTKRILDEKOOHIV 76

Qy 61 CSNDLIGDLFGVPSFSVKEHRKITYTMIYRNLVYVQESSDSGTYSSEN 109  
 Db 77 CSNDLIGDLFGVPSFSVKEHRKITYMVLVAVSQ---DSGTISLES 122

RESULT 12  
 US-09-966-724-4  
 Sequence 4, Application US/09966724  
 Publication No. US2004017071A1  
 GENERAL INFORMATION:  
 APPLICANT: THE JOHNS HOPKINS UNIVERSITY  
 ADDRESS: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA  
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN HUMAN TUMORS  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 STREET: 1001 G ST., N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20001-4597

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.2.5

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/966,724  
 FILING DATE: 01-OCT-2001  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/044,619  
 FILING DATE: 2001-10-01  
 APPLICATION NUMBER: US 07/867,840  
 FILING DATE: 07-APR-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KAGAN, SARAH A.  
 REGISTRATION NUMBER: 32,141  
 REFERENCE/DOCKET NUMBER: 01107.40148  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-508-9100  
 TELEX: 197430 BBMB UT  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 489 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-966-724-4

Query Match 88.2%; Score 488.5; DB 11; Length 489;  
 Best Local Similarity 87.2%; Pred. No. 3.3e-49;  
 Matches 95; Conservative 8; Mismatches 3; Indels 3; Gaps 1;

Query 1 SQTIPASEQETLVRPKPLILKLUKSVAQKDVTMKEVLFYLGQYIMTRKLYDEKQHIVYH 60  
 Database 17 SQTIPASEQETLVRPKPLILKLUKSVAQKDVTMKEVLFYLGQYIMTRKLYDEKQHIVYH 76

Query 61 CSNDLIGDLEGYPSFSVKEHRKITYMIRNLVNVNQESSSDSGTSESN 109  
 Database 77 CSNDLIGDVGYPSPFSVKEHRKITYMIRNLVAVSQ--DSGTSLES 122

RESULT 13 US-10-685-838-2  
 ; Sequence 2, Application US/10685838  
 ; Publication No. US20040197893A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHUBERT, CARSTEN  
 ; APPLICANT: GRASBERGER, BRUCE  
 ; APPLICANT: MAGUIRE, DIANE  
 ; APPLICANT: DECKMAN, INGRID  
 ; APPLICANT: SPURLINO, JOHN  
 ; TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF  
 ; FILE REFERENCE: PRD-2137-USANP  
 ; CURRENT APPLICATION NUMBER: US/10/685,838  
 ; CURRENT FILING DATE: 2003-10-15  
 ; PRIOR APPLICATION NUMBER: 60/418,350  
 ; PRIOR FILING DATE: 2002-10-16  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn Ver. 3.2  
 ; SEQ ID NO: 2  
 ; LENGTH: 95  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-685-838-2

Query Match 86.4%; Score 481; DB 16; Length 95;  
 Best Local Similarity 98.9%; Pred. No. 3e-49; Indels 0; Gaps 0;  
 Matches 94; Conservative 1; Mismatches 0; Gaps 0;

Query 1 SQTIPASEQETLVRPKPLILKLUKSVAQKDVTMKEVLFYLGQYIMTRKLYDEKQHIVYH 60  
 Database 1 SQTIPASEQETLVRPKPLILKLUKSVAQKDVTMKEVLFYLGQYIMTRKLYDEKQHIVYH 60

Query 61 CSNDLIGDLEGYPSFSVKEHRKITYMIRNLVNVN 95  
 Database 61 CSNDLIGDVGYPSPFSVKEHRKITYMIRNLVNVN 95

RESULT 14 US-10-685-838-4  
 ; Sequence 4, Application US/10685838  
 ; Publication No. US20040197893A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHUBERT, CARSTEN  
 ; APPLICANT: GRASBERGER, BRUCE  
 ; APPLICANT: MAGUIRE, DIANE  
 ; APPLICANT: DECKMAN, INGRID  
 ; APPLICANT: SPURLINO, JOHN  
 ; TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF  
 ; FILE REFERENCE: PRD-2137-USANP  
 ; CURRENT APPLICATION NUMBER: US/10/685,838  
 ; CURRENT FILING DATE: 2003-10-15  
 ; PRIOR APPLICATION NUMBER: 60/418,350  
 ; PRIOR FILING DATE: 2002-10-16  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn Ver. 3.2  
 ; SEQ ID NO: 4  
 ; LENGTH: 95  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-685-838-4

Query Match 85.2%; Score 472; DB 16; Length 95;  
 Best Local Similarity 97.9%; Pred. No. 3.5e-48; Indels 0; Gaps 0;

Search completed: February 16, 2005, 08:50:04  
 Job time : 698 secs

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OM protein - protein search, using sw model

Run on: February 16, 2005, 08:21:05 ; Search time 38 Seconds  
(without alignments)

275.990 Million cell updates/sec

Title: US-10-822-254-6

Perfect score: 554

Sequence: 1 SQIPASEQETLVPRPKPLIK. .... .NLVVVNQQESSDGGTSEEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79;\*

1: pir1;\*

2: pir2;\*

3: pir3;\*

4: pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	548	98.9	491	1	S24354		p53-binding protein
2	488.5	88.2	489	2	S24349		mdm2-like p53-binding protein
3	271.5	49.0	489	2	S71955		MDM2-like p53-binding protein
4	94	15.2	695	1	SXBPT4		NAD+-protein ADP-R
5	84	15.2	698	1	S31630		NAD+-protein ADP-R
6	73.5	13.3	698	1	S31714		NAD+-protein ADP-R
7	73.5	13.3	467	2	T25848		hypothetical protein
8	72.5	13.1	565	2	S2682		hypothetical protein
9	72.5	13.1	2833	2	A43360		inositol 1,4,5-tri
10	72	13.0	967	2	A64710		typ III restricti
11	71.5	12.9	514	2	B65169		hypothetical prote
12	70.5	12.7	709	2	B64213		DNA topoisomerase
13	70.5	12.7	838	2	I45557		eyeless, long form
14	70	12.6	969	2	E71810		type III restricti
15	68	12.3	134	2	G63382		response regulator
16	67	12.1	176	2	JQ1813		B19R protein - vac
17	67	12.1	181	2	S75415		probable ribosomal
18	67	12.1	261	2	H71680		exodeoxyribonuclea
19	67	12.1	3092	2	S46009		GTPase-activating
20	66.5	12.0	422	2	T26334		hypothetical prote
21	66.5	12.0	447	2	I64002		sodium-translocati
22	66.5	12.0	517	2	S32169		hypothetical prote
23	65.5	11.8	277	2	A10589		conserved hypothet
24	65.5	11.8	339	2	A90395		conserved hypothet
25	65.5	11.8	425	2	T50184		mammalian swi/snf
26	65.5	11.8	450	2	G7025		conserved hypothet
27	65.5	11.8	704	2	H82381		toxin secretion AT
28	65	11.7	232	2	E89501		hypothetical prote
29	65	11.7	260	2	T28182		hypothetical prote

## RESULT 1

S24354  
p53-binding protein mdm2 - human  
N;Alternate names: mdm-2 oncogene; mouse double minute 2 homolog; p53-associated phospho  
C;Species: Homo sapiens (man)  
C;Date: 17-Mar-2000 #sequence revision 17-Mar-2000  
C;Accession: S24354; SS5738; G02026  
R;Oliner, J.D.; Kinzler, K.W.; Meltzer, P.S.; George, D.L.; Vogelstein, B.  
Nature 358, 80-83, 1992  
A;Title: Amplification of a gene encoding a p53-associated protein in human sarcomas.  
A;Reference number: S24354; MUID:93310576; PMID:1614537  
A;Accession: S24354  
A;Molecule type: mRNA  
A;Residues: 1-91 '>OLI>  
R;Zauberman, A.; Plusberg, D.; Haupt, Y.; Barak, Y.; Oren, M.  
Nucleic Acids Res. 23, 2384-2392, 1995  
A;Title: A functional p53-associated protein is contained within the human mdu  
A;Reference number: SS5738; MUID:7651818  
A;Accession: SS7338  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-16,'P'18-24 <ZAU>  
A;Cross-references: EMBL:U28945; NID:9904033; PIDN:AAA622371; PMID:9904034  
R;Lunec, J.  
submitted to the EMBL Data Library, August 1995  
A;Description: Multiple alternate spliced mdm2 transcripts with loss of p53 binding domain  
A;Reference number: G09070  
A;Accession: G02026  
A;Molecule type: mRNA  
A;Residues: 1-27,223-491 <UNP>  
A;Cross-references: EMBL:U33199; NID:9992676; PIDN:AAA755141; PMID:9992677  
A;Experimental source: splice form A  
C;Genetics:  
A;Gene: G63:MDM2  
A;Cross-references: GDB:250456; OMIM:164785  
A;Map position: 12q14.3-12q15  
C;Superfamily: human p53-binding protein mdm2  
C;Keywords: alternative splicing; oncogene; phosphoprotein  
F;1-491/Product: p53-binding protein mdm2 #status predicted <MAT1>  
F;1-27,223-491/Product: p53-binding protein mdm-2, splice form A #status predicted <MAT1>  
P;1-27,223-491/Product: p53-binding protein mdm-2, splice form A #status predicted <MAT1>

Query Match 98.9%; Score 548; DB: 1; Length 491;  
Best Local Similarity 99.1%; Pred. No. 5e-49;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SQIPASEQETLVPRPKPLIKSVAQKDVTYMKVLYFLYQYIMTKRLYDEKQHIVH 60  
Db 17 SQIPASEQETLVPRPKPLIKSVAQKDVTYMKVLYFLYQYIMTKRLYDEKQHIVY 76

Qy 61 CSNDLIGDLFGVPSFSYKEHRKITYMIRNLVYVNQESSSDSGTSVSEN 109  
 Db 77 CSNDLIGDLFGVPSFSYKEHRKITYMIRNLVYVNQESSSDSGTSVSEN 125

## RESULT 2

S15349 protein - mouse

C;Species: Mus musculus (house mouse)

C;Accession: S15349 Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

R;Fakharzad, S.S.; Trusko, S.P.; George, D.L.

A;Title: Tumorigenic potential associated with enhanced expression of a gene that is am-

A;Reference number: S15349; MUID:91224107; PMID:2056149

A;Cross-references: UNIPROT:P23804; EMBL:X58876; NID:g53038; PID:CAA41684\_1; PID:g53039

A;Genetics: A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-489 <SHR>

A;Accession: S15349

C;Superfamily: p53-binding protein mdm2

Query Match Score 88.2%; Best Local Similarity 87.2%; Pred. No. 7.4e-43; Length 489;

Matches 95; Conservative 8; Mismatches 3; Indels 3; Gaps 1;

Db 17 SQQPASEDTLYRKPLKLKLSVGAAQDKDTYTMKEVLIFYLQGXTMTKRLYDEKQOHIVH 60

Qy 61 CSNDLIGDLFGVPSFSYKEHRKITYMIRNLVYVNQESSSDSGTSVSEN 109

Db 77 CSNDLIGDLFGVPSFSYKEHRKITYMIRNLVYVNQESSSDSGTSVSEN 122

## RESULT 3

S71955 MDM2-like p53-binding protein MDMX - mouse

C;Species: Mus musculus (house mouse)

C;Accession: S71955 Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 09-Jul-2004

R;Shvarts, A.; Steegenga, W.T.; Riteco, N.; van Laar, T.; Dekker, P.; Bazuine, M.; van H

EMBO J 15: 5349-5357, 1996

A;Title: MDMX: a novel p53-binding protein, with some functional properties of MDM2.

A;Reference number: S71955; MUID:97050840; PMID:8995579

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-489 <SHR>

A;Cross-references: UNIPROT:O35618; EMBL:AF007110; NID:g225338; PID:AA62927\_1; PID:g2

C;Genetics: A;Gene: MDMX

C;Function: inhibits transcription activation function of tumour suppressor protein p

C;Superfamily: human p53-binding protein mdm2

Query Match Score 49.0%; Best Local Similarity 52.4%; Pred. No. 2.4e-20; Length 489;

Matches 55; Conservative 17; Mismatches 22; Indels 11; Gaps 1;

Db 20 SSEQETLYRKPLKLKLSVGAAQDKDTYTMKEVLIFYLQGXTMTKRLYDEKQOHIVHCSND 64

Qy 5 LIGDLFGVPSFSYKEHRKITYMIRNLVYVNQESSSDSGTSVSEN 109

Db 80 LIGDLFGVPSFSYKEHRKITYMIRNLVYVNQESSSDSGTSVSEN 113

## RESULT 6

S31714 NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T6

C;Species: phage T6

C;Accession: S31714 Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

R;Rueger, W. submitted to the EMBL Data Library, December 1992

A;Title: Sequencing of the ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of

A;Reference number: S31630

A;Accession: S31630 C;Superfamily: phage T4 NAD+-protein ADP-ribosyltransferase

C;Keywords: Glycosyltransferase; NAD; Pentosyltransferase

A;Molecule type: DNA

A;Residues: 1-698 <KOC>

A;Cross-references: UNIPROT:038424; EMBL:X69893; NID:g15187; PID:CAA49517\_1; PID:g15188

C;Genetics: A;Gene: preliminary

C;Function: phage T4 NAD+-protein ADP-ribosyltransferase

C;Status: translation not shown

C;Accession: S31630

C;Keywords: Glycosyltransferase; Pentoxylyltransferase

A;Molecule type: DNA

A;Residues: 1-885

A;Cross-references: UNIPROT:P12726

C;Comment: This enzyme catalyzes the ADP-ribosylation of one of the two alpha-subunits o

C;Genetics: C;Superfamily: phage T4 NAD+-protein ADP-ribosyltransferase

C;Keywords: Glycosyltransferase; Pentoxylyltransferase

A;Molecule type: DNA

A;Accession: S31630

C;Cross-references: UNIPROT:P12726

C;Comment: This enzyme catalyzes the ADP-ribosylation of one of the two alpha-subunits o

NAD+-Protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T4

C;Species: phage T4

C;Accession: S31714

C;Status: host: Escherichia coli

C;Function: #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004

R;Hilse, D.; Rueger, W.

Nucleic Acids Res. 17, 6731, 1989

A;Title: Nucleotide sequence of the alt gene of bacteriophage T4.

A;Reference number: JU0056

A;Accession: JU0056

A;Status: translation not shown

C;Accession: JU0056

A;Keywords: Glycosyltransferase

A;Molecule type: DNA

A;Residues: 1-885

A;Cross-references: UNIPROT:ADP-ribosyltransferase #status predicted <MAT>

C;Genetics: C;Superfamily: phage T4 NAD+-protein ADP-ribosyltransferase

C;Keywords: Glycosyltransferase; Pentoxylyltransferase

A;Molecule type: DNA

A;Accession: S31630

C;Cross-references: UNIPROT:ADP-ribosyltransferase #status predicted <MAT>

C;Genetics: C;Superfamily: phage T4 NAD+-protein ADP-ribosyltransferase

C;Keywords: Glycosyltransferase; Pentoxylyltransferase

A;Molecule type: DNA

A;Accession: S31630

C;Cross-references: UNIPROT:ADP-ribosyltransferase #status predicted <MAT>

C;Genetics: C;Superfamily: phage T4 NAD+-protein ADP-ribosyltransferase

C;Keywords: Glycosyltransferase; Pentoxylyltransferase

A;Molecule type: DNA

A;Accession: S31630

C;Cross-references: UNIPROT:ADP-ribosyltransferase #status predicted <MAT>

C;Genetics: C;Superfamily: phage T4 NAD+-protein ADP-ribosyltransferase

C;Keywords: Glycosyltransferase; Pentoxylyltransferase

A;Molecule type: DNA

A;Accession: S31630

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C;Keywords: Glycosyltransferase; Pentoxylyltransferase

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C;Keywords: Glycosyltransferase; Pentoxylyltransferase

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C;Keywords: Glycosyltransferase; Pentoxylyltransferase

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C;Cross-references: UNIPROT:ADP-ribosyltransferase #status predicted <MAT>

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C;Keywords: Glycosyltransferase; Pentoxylyltransferase

A;Molecule type: DNA

A;Accession: S31630

C;Cross-references: UNIPROT:ADP-ribosyltransferase #status predicted <MAT>

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C;Keywords: Glycosyltransferase; Pentoxylyltransferase

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A;Accession: S31630

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A;Accession: S31630

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C;Keywords: Glycosyltransferase; Pentoxylyltransferase

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C;Keywords: Glycosyltransferase; Pentoxylyltransferase

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A;Accession: S31630

C;Cross-references: UNIPROT:ADP-ribosyltransferase #status predicted <MAT>

C;Genetics: C;Superfamily: phage T4 NAD+-protein ADP-ribosyltransferase

A;Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of  
A;Reference number: S31630  
A;Accession: S31714  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-658 <ROC>  
A;Cross-references: UNIPROT:Q38433; EMBL:X69894; NID:915422; PID:CAA49518.1; PID:915423  
C;Superfamily: phage T4 NAD-protein ADP-ribosyltransferase  
C;Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 15.2%; Score 84; DB 1; Length 698;  
Best Local Similarity 29.0%; Pred. No. 1;  
Matches 29; Conservative 22; Mismatches 35; Indels 14; Gaps 6;

Qy 18 LLKLLKSG-VGAQKDTYTMKEVLFYL--GQYIMTKRL--YDEKQQHQI-YHCSNDLIGDL 69  
Db 112 MURILIKSTAGQARQIQVIAIDLRSRSGGRYVLLKELWDYDKKTYAYLTHKNTVSLEDI 171

RESULT 7

Qy 70 FGVPSFSVKEHRKITYMVLNLUVVAQEQSSSDGTSVSEN 109  
Db 172 PGVPEISTELFTPKVESKV--GTDVYINK---DTGAQVTRN 205

RESULT 7

T5848 hypothetical protein T01B11.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Accession: T28848  
R;Geisel, C.; Stellyes, L.  
Submitted to the EMBL Data Library, December 1996  
A;Description: the sequence of C. elegans cosmid T01B11.  
A;Reference number: Z20099  
A;Accession: T28848  
A;Status: Preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: DNA  
A;Residues: 1-467 <GBI>  
A;Cross-references: UNIPROT:P91408; EMBL:U80931; PIDN:AAB37999.1; GSPDB:GN000222; CESP:TO01B11  
A;Experimental source: strain Bristol N2; clone T01B11  
C;Genetics:

Query Match 13.3%; Score 73.5; DB 2; Length 467;  
Best Local Similarity 32.9%; Pred. No. 7.7;  
Matches 25; Conservative 5; Mismatches 25; Indels 21; Gaps 3;

Qy 1 SOIPASEQETLYRPKPLKLKLSVGQKDTYTMKEVLFYLQCYIMTKR----LYDEKQ 55  
Db 13 SSTOPAAKTRDYSKELI-----RRDITIGSKQIFYSDDPFWRSRASMQIYDEK 66

RESULT 10

Qy 56 -----OHIWHC 61  
Db 67 NRFLDC1S1SVQFVGHC 82

RESULT 8

S52682 hypothetical protein YDR117C - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein YD9727.12C  
C;Species: Saccharomyces cerevisiae  
C;Accession: SS195  
R;Murphy, L.; Shore, L.; Harris, D.  
Submitted to the EMBL Data Library, March 1995  
A;Reference number: SS2671  
A;Accession: S52682  
A;Molecule type: DNA  
A;Residues: 1-565 <MTR>  
A;Cross-references: UNIPROT:Q04600; EMBL:Z48758; NID:9747879; PID:9747891; GSPDB:GN00004

A;Gene: MIPS:YDR117C  
A;Cross-references: SGD:S0002524  
A;Map position: 4R

Query Match 13.1%; Score 72.5; DB 2; Length 565;  
Best Local Similarity 33.3%; Pred. No. 12;  
Matches 25; Conservative 11; Mismatches 30; Indels 9; Gaps 3;

Qy 10 TLVPRPKPLKLKLSVGQKDTYTMKEVLFYLQCYIMTKRLYDEKQQHQIYHCSNDLIGDL 68  
Db 362 TLYKPPNLARDLKLKEYNLASHTYYTSQDIRSAVQOTISVKNLADTxDKGKV-IMDDILFD 420

Qy 69 LFGVPSFSVKEHRKI 83  
Db 421 M-----VNKKKKV 428

RESULT 9

A43360 inositol 1,4,5-trisphosphate receptor - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A43360  
R;Yoshikawa, S.; Tanimura, T.; Miyawaki, A.; Nakamura, M.; Furuchi, T.; Mikl, J. Biol. Chem. 267, 1661-1669, 1992  
A;Title: Molecular cloning and characterization of the inositol 1,4,5-trisphosphate receptor  
A;Reference number: A43360; PMID:92355637; PMID:1122910  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-2833 <YOS>  
A;Cross-references: UNIPROT:P29993; GB:D90403; NID:9217337; PIDN:BAAl4399.1; PID:9217338  
A;Note: Sequence extracted from NCBI backbone (NCBIP:111077)  
C;Keywords: transmembrane protein  
C;Genetics:  
A;Gene: FlyBase:Ityp-r83A  
A;Cross-references: FlyBase:FBgn0010051  
C;Superfamily: inositol-trisphosphate receptor

Query Match 13.1%; Score 72.5; DB 2; Length 2833;  
Best Local Similarity 24.3%; Pred. No. 79;  
Matches 26; Conservative 25; Mismatches 37; Indels 19; Gaps 4;

Qy 3 IPASEQETLYRPKPLKLKLSVGAA-----QKDTYMKVFLYLGQYIMTKR 49  
Db 1286 VTASGPSSVVRPRHQRQLLNQVGETVVLQNPYDEKDELMCLAEFLONFC 1345

Query Match 13.1%; Score 72.5; DB 2; Length 2833;  
Best Local Similarity 24.3%; Pred. No. 79;  
Matches 26; Conservative 25; Mismatches 37; Indels 19; Gaps 4;

Qy 50 LYDEKQHIVYCNSNDLIGDLFGVPSSVKERKITYMIRLYVNNQ 96  
Db 1346 LGNOQNQVLHH-NHHL-DLEFLNPNP-GILEAKTVAIFKONLALCNE 1386

RESULT 10

A64710 type III restriction enzyme R protein - Helicobacter pylori (strain 26695)  
C;Species: Helicobacter pylori  
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: A64710  
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenna, R.; Tomb, J.F.; Weidman, J.M.; Cottrell, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Son, J.D.; Kelley, J.M.; Cottrell, M.D.; Weidman, J.M.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.;Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.;Reference number: A64520; PMID:97394467; PMID:9252185  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-367 <TOM>  
A;Cross-references: UNIPROT:Q26050; GB:AE000650; GB:AE000511; NID:92314700; PIDN:ADD005<  
C;Genetics:  
A;Start codon: GTG



Db 770 NEIRKNEOEGLKRLEELPLEIYQNIKDKISYQMRETT-----IKNRKNDAYFYDEKGEE- 822  
 Qy 58 IVHCSNDLIGDGFVPSFSVKEHRKITYMIVNLYVNNQQESSSDS 102  
 Db 823 ---IREFLDGSUIGADKYEIKXNSAQEKCILYENFMQVSETEKDT 863

## RESULT 15

G69382

responsible regulator homolog - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Gildek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woesz, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: G69382

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-134 &lt;KUE&gt;

A;Cross-references: UNIPROT:O29199; GB:AE001029; PIDN:92689352; PIDN:AAB9017

C;Superfamily: signal transduction receiver (phosphoacceptor) protein, CheY type; respon

C;Keywords: phosphoprotein

P;20-126/Domain: response regulator homology &lt;RRH&gt;

P;66/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 12.3%; Score 68; DB 2; Length 134;

Best Local Similarity 28.4%; Pred. No. 6 8;

Matches 21; Conservative 15; Mismatches 38; Indels 0; Gaps 0;

Qy 35 KEVLFYLGQYINTKRLYDKQQHQHIVHCSNDLIGDLFGVPSFSVKERKITYMIVRNLYVV 94  
 | : ||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 6 KELPFWHLHPNIMTKILVDDDCSICELYKEILGSFEVVACSGREGHELYRKLMPPDVIV 65

Qy 95 NQOESSSSGTGTSSE 108

| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 66 DINMPDTSGVEVAK 79Search completed: February 16, 2005, 08:24:51  
 Job time : 41 sec

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Copyright	GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.	protein - protein Search, using bw model	on:	February 16, 2005, 08:21:05 ; Search time 170 seconds (without alignment(s)) 328.333 Million cell updates/sec	Score:	US-10-822-254-6	Effect score:	554	Sequence:	1 SQIPASEQETLVPRPKPLIKK. .... .NLVVTNQQESSSDSGTCSVSEN 109	String table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	Number of hits satisfying chosen parameters:	1612378	Result 1	Q8NDW2	PRELIMINARY;	PRT;	166 AA.
															AC	Q8NDW2;				
															DT	01-OCT-2002	(TREMBLrel.	22,	Created)	
															DT	01-OCT-2002	(TREMBLrel.	22,	Last sequence update)	
															DT	01-JUN-2003	(TREMBLrel.	24,	Last annotation update)	
															DB	P53-binding protein.				
															GN	Name=MDM2;				
															OS	Homo sapiens (Human)				
															OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
															OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
															[1]	SEQUENCE FROM N.A.				
															RA	Bartel F., Pinkel D., Kappeler M., Bache M., Schmidt H., Taubert H.;				
															RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.				
															DR	EMBL; AJ491698; CAD36395.1; -.				
															DR	HSSP; Q9UMTB8; LYCR.				
															DR	GO; GO:0005734; C:nucleus; IEA.				
															DR	InterPro; IPR001984; MDM2.				
															DR	InterPro; IPR003121; SWIB_MDM2.				
															DR	Pfam; PF02201; SWIB; 1.				
															SQ	SEQUENCE 166 AA; SWIB; 1.				
															RN	SEQUENCE FROM N.A.				
															RP	Barzel F., Pinkel D., Kappeler M., Bache M., Schmidt H., Taubert H.;				
															NCBI_TaxID=9606;	[1]	SEQUENCE FROM N.A.			
															RN	SEQUENCE FROM N.A.				
															RA	Barzel F., Pinkel D., Kappeler M., Bache M., Schmidt H., Taubert H.;				
															RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.				
															DR	EMBL; AJ491698; CAD36395.1; -.				
															DR	HSSP; Q9UMTB8; LYCR.				
															DR	GO; GO:0005734; C:nucleus; IEA.				
															DR	InterPro; IPR001984; MDM2.				
															DR	InterPro; IPR003121; SWIB_MDM2.				
															DR	Pfam; PF02201; SWIB; 1.				
															RN	SEQUENCE 166 AA; SWIB; 1.				
															RP	SEQUENCE FROM N.A.				
															NCBI_TaxID=9606;	[1]	SEQUENCE FROM N.A.			
															RN	SEQUENCE FROM N.A.				
															RP	SEQUENCE FROM N.A.				
															RC	TISSUE=Rhabdomyosarcoma tumor;				
															RC	TISSUE=Rhabdomyosarcoma tumor;				

RA Bartel P., Taylor A.C., Taubert H., Harris L.C.;  
Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR DR HSSP; Q9UMT8; AF385223; AAL13243; 1; -.

DR DR GO; GO:0005634; 1YCR.

DR DR InterPro; IPR010384; MDM2.

DR DR InterPro; IPR003121; SWIB\_MDM2.

DR PRAM; PF02201; SWIB; 1.

SEQ SEQUENCE 195 AA; 22161 MW; 4987AF567DB12D5D CRC64;

Query Match Score 98.9%; Score 548; DB 2; Length 195;

Best Local Similarity 99.1%; Pred. No. 8 5e-51; ;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVH 60

Db 17 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVY 76

Qy 61 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 109

Db 77 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 125

### RESULT 3

Q8TE47 PRELIMINARY; PRT; 243 AA.

AC ID Q8TE47; PRELIMINARY; PRT; 243 AA.

DT DT 01-JUN-2002 (TRNBLrel. 21; Created)

DT DT 01-JUN-2003 (TRNBLrel. 21; Last sequence update)

DT DT 01-JUN-2003 (TRNBLrel. 24; Last annotation update)

DR DR MDM2 isoform KB9 protein.

GN GN Name=MDM2 isoform KB9;

OS OS Homo sapiens (Human).

OC OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN RN NCBI\_TaxID=9606;

RP RP SEQUENCE FROM N.A.

RC TISSUE=Lymphocytes;

RA RA Bartel P., Pinkert D., Kappeler M., Baché M., Schmidt H., Taubert H.;

RL RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR DR EMBL; AJ430612; CAD2;251.; -.

DR DR HSSP; Q9UMT8; 1YCR.

DR DR GO; GO:0005634; C:nucleus; IEA.

DR DR GO; GO:000151; C:ubiquitin ligase complex; IEA.

DR DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

DR DR GO; GO:0005270; SWIB; 1; -.

DR DR GO; GO:0016567; F:protein ubiquitination; IEA.

DR DR InterPro; IPR010984; MDM2.

DR DR InterPro; IPR003121; SWIB\_MDM2.

DR DR InterPro; IPR001841; Znf\_Fing.

DR DR SMART; SM00184; RING\_1.

DR DR PROSITE; PS50089; ZF\_RING\_2; 1.

SQ SQ SEQUENCE 243 AA; 27317 MW; 9EB5D0142GF185A2 CRC64;

Query Match Score 98.9%; Score 548; DB 2; Length 243;

Best Local Similarity 99.1%; Pred. No. 1.e-50; ;

Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVH 60

Db 17 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVY 76

Qy 61 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 109

Db 77 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 125

RESULT 4  
MDM2\_HUMAN STANDARD PRT; 491 AA.  
AC Q00987; Q13226; Q13297; Q13300; Q13301; Q9UGI3;

AC Q9UMT8;	DT 01-APR-1993 (Rel. 25, Created)
DR DR HSSP; Q9UMT8; 1YCR.	DT 01-APR-1993 (Rel. 25, Last sequence update)
DR DR GO; GO:0005634; C:nucleus; IEA.	DT 25-OCT-2004 (Rel. 45, Last annotation update)
DR DR InterPro; IPR010384; MDM2.	DR Ubiquitin-Protein Ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Hdm2). Name=MDM2;
DR DR InterPro; IPR003121; SWIB_MDM2.	GN OS Homo sapiens (Human).
DR PRAM; PF02201; SWIB; 1.	OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
SEQ SEQUENCE 195 AA; 22161 MW; 4987AF567DB12D5D CRC64;	NCBI_TaxID=9606;
Query Match Score 98.9%; Score 548; DB 2; Length 195;	OX OX
Best Local Similarity 99.1%; Pred. No. 8 5e-51; ;	RN RN
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	RP RP
Qy 1 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVH 60	SEQUENCE FROM N.A. (ISOFORM MDM2).
Db 17 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVY 76	MEDLINE=9210576; PubMed=161337;
Qy 61 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 109	Oliner J.D., Kanzler K.W., Meltzer D.L., George D.L., Vogelstein B.;
Db 77 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 125	"Amplification of a gene encoding a p53-associated protein in human sarcomas." Nature 358:80-83 (1992).
Query Match Score 98.9%; Score 548; DB 2; Length 195;	[1] [2]
Best Local Similarity 99.1%; Pred. No. 8 5e-51; ;	RN RN
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	RC RC
Qy 1 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVH 60	SEQUENCE FROM N.A. (ISOFORMS MDM2-A; -B; -C; -D AND -E).
Db 17 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVY 76	MEDLINE=9613107; PubMed=9705662;
Qy 61 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 109	TISSUE=Ovarian carcinoma;
Db 77 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 125	MEDLINE=9631307; PubMed=9705662;
Query Match Score 98.9%; Score 548; DB 2; Length 195;	[3]
Best Local Similarity 99.1%; Pred. No. 8 5e-51; ;	RN RN
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	RA RA
Qy 1 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVH 60	SEQUENCE FROM N.A. (ISOFORM MDM2-ALPHA).
Db 17 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVY 76	MEDLINE=20065171; PubMed=10597303; DOI=10.1038/sj.onc.1203182;
Qy 61 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 109	Signals I.; Calvert A.H.; Anderson J.J.; Neal D.E.; Lunec J.;
Db 77 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 125	"Alternatively spliced mdm2 transcripts with loss of p53 binding domain sequences: transforming ability and frequent detection in human cancer." Nat. Med. 2:912-917 (1996).
Query Match Score 98.9%; Score 548; DB 2; Length 195;	[4]
Best Local Similarity 99.1%; Pred. No. 8 5e-51; ;	RN RN
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	RA RA
Qy 1 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVH 60	SEQUENCE FROM N.A. (ISOFORM MDM2).
Db 17 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVY 76	MEDLINE=22388227; PubMed=12477932; DOI=10.1073/pnas.242260389;
Qy 61 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 109	Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
Db 77 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 125	Nguyen D.A., Poel C.L., Robertson P.D.,
Query Match Score 98.9%; Score 548; DB 2; Length 195;	[5]
Best Local Similarity 99.1%; Pred. No. 8 5e-51; ;	RA RA
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	RA RA
Qy 1 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVH 60	SEQUENCE FROM N.A. (ISOFORM MDM2).
Db 17 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVY 76	MEDLINE=22388227; PubMed=12477932; DOI=10.1073/pnas.242260389;
Qy 61 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 109	Riede M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
Db 77 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 125	Nguyen D.A., Poel C.L., Robertson P.D.,
Query Match Score 98.9%; Score 548; DB 2; Length 195;	[6]
Best Local Similarity 99.1%; Pred. No. 8 5e-51; ;	RA RA
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	RA RA
Qy 1 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVH 60	SEQUENCE FROM N.A. (ISOFORM MDM2).
Db 17 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVY 76	MEDLINE=22388227; PubMed=12477932; DOI=10.1073/pnas.242260389;
Qy 61 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 109	Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
Db 77 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 125	Nguyen D.A., Poel C.L., Robertson P.D.,
Query Match Score 98.9%; Score 548; DB 2; Length 195;	[7]
Best Local Similarity 99.1%; Pred. No. 8 5e-51; ;	RA RA
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	RA RA
Qy 1 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVH 60	SEQUENCE OF 6-491 FROM N.A. (ISOFORM MDM2-A).
Db 17 SQIPASEQDTLYRPKPLKLKLSVGAQKDVTMKEVLFYLGQYIMTRKLYDEKQOHIVY 76	Liang H., Atkins H., Abel-Fattah R., Suayun R., Lunec J.;
Qy 61 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 109	"Genomic organisation of the human MDM2 oncogene and relationship to its alternative spliced mRNA's";
Db 77 CSNDLGLGFLGPYSFSVKEHRKLYTMYRNLYVNNOEESSDSGTSYSEN 125	Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

SEQUENCE OF 1-24 FROM N.A.; MEDLINE=9530270; PubMed=7651818;  
 RX Zauberman A., Flusberg D.; Haupt Y., Barak Y., Oren M.;  
 RA "A functional p53-responsive intronic promoter is contained within the  
 RT human mdm2 gene.";  
 RL Nucleic Acids Res. 23:2584-2592(1995).  
 RN [8]

SEQUENCE OF 1-9 FROM N.A.; MEDLINE=97413643; PubMed=9270029;  
 RX Landers J.E., Caselli S.L., George D.L.;  
 RA "Translational enhancement of mdm2 oncogene expression in human tumor  
 RT cells containing a stabilized wild-type p53 protein.";  
 RL Cancer Res. 57:3562-3568(1997).  
 RN [9]

SEQUENCE OF 301-481 FROM N.A.  
 MEDLINE=20542019; PubMed=11087994; DOI=10.1016/S0027-5107(00)00112-3;  
 RX Taubert H., Kappeler M., Meyer A., Bartel P., Schliott T.,  
 RA Lautenschlaeger C., Baché M., Schmidt H., Wuerl P.;  
 RT "A MboII polymorphism in exon 11 of the human MDM2 gene occurring in  
 normal blood donors and in soft tissue sarcoma patients: an indication  
 RT for an increased cancer susceptibility?";  
 RL Mutat. Res. 456:39-44 (2000).  
 RN [10]

RX MUTAGENESIS OF CYS-464.  
 MEDLINE=98111004; PubMed=9450543; DOI=10.1016/S0014-5793(97)01480-4;  
 RX Honda R., Tanaka H., Yasuda H.;  
 RA "Oncoprotein MDM2 is a ubiquitin ligase E3 for tumor suppressor p53.";  
 RT "Activity of MDM2, a ubiquitin ligase, toward p53 or itself is  
 RL dependent on the RING finger domain of the ligase.";  
 RN [11]

RX MUTAGENESIS OF CYS-449.  
 MEDLINE=20190101; PubMed=10723139; DOI=10.1038/sj.onc.1203464;  
 RX Honda R., Yasuda H.;  
 RA "Activity of MDM2, a ubiquitin ligase, toward p53 or itself is  
 RT dependent on the RING finger domain of the ligase.";  
 RN [12]

RX MUTAGENESIS.  
 MEDLINE=20187618; PubMed=10722742; DOI=10.1074/jbc.275.12.8945;  
 RA Fang S., Jensen J.P., Ludwig R.L., Voussen K.H., Weissman A.M.;  
 RT "MDM2 is a RING finger-dependent ubiquitin protein ligase for itself  
 RT and p53.";  
 RL J. Biol. Chem. 275:8945-8951(2000).  
 RN [13]

RX MUTAGENESIS OF CYS-441 AND CYS-478.  
 MEDLINE=20076498; PubMed=10608992; DOI=10.1074/jbc.274.53.38189;  
 RA Sharp D.A., Kratowicz S.A., Sank M.J., George D.L.;  
 RT "Stabilization of the MDM2 oncoprotein by interaction with the  
 structurally related MDMX protein";  
 RL J. Biol. Chem. 274:38189-38196 (1999).  
 RN [14]

RX NUCLEOLAR LOCALIZATION SIGNAL.  
 MEDLINE=20073879; PubMed=10103090; DOI=10.1038/35004057;  
 RA "Identification of a cryptic nucleolar-localization signal in MDM2.";  
 RL Nat. Cell Biol. 2:179-181(2000).  
 RN [15]

RX PHOSPHORYLATION BY ATM.  
 MEDLINE=20079519; PubMed=10611322; DOI=10.1073/pnas.96.26.14973;  
 RA Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;  
 RT "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation  
 in response to DNA damage";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977 (1999).  
 RN [16]

X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 25-109 IN COMPLEX WITH P53.  
 RX MEDLINE=97081050; PubMed=875929; DOI=10.1126/science.274.5289.948;  
 RA Kussie P.H., Gorina S., Marechal V., Elmenbaas B., Moreau J.,  
 Levine A.J., Pavletich N.P.;  
 RT "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor  
 transactivation domain.";  
 RL Science 274:948-953 (1996).  
 CC "- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and  
 CC apoptosis by binding its transcriptional activation domain.  
 CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,

toward p53 and itself. Permits the nuclear export of p53 and  
 targets it for proteasome-mediated proteolysis.  
 COFACTOR: Zinc is required for ubiquitin ligase E3 activity.  
 SUBUNIT: Binds p53, p73, ARF (p14), ribosomal protein L5 and  
 (BB), E1A-associated protein EP300 and the E2F1 transcription  
 factor.  
 SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed  
 predominantly in the nucleoplasm. Interaction with ARF (p14)  
 results in the localization of both proteins to the nucleolus. The  
 nucleolar localization signals in both ARF (p14) and MDM2 may be  
 necessary to allow efficient nucleolar localization of both  
 proteins.  
 ALTERNATIVE PRODUCTS:  
 Event-Alternative splicing; Named isoforms=8;  
 Name=Mdm2;  
 IsoId=Q00987-1; Sequence=Displayed;  
 Name=Mdm2-A;  
 IsoId=Q00987-2; Sequence=VSP\_003208;  
 Name=Mdm2-Al;  
 IsoId=Q00987-3; Sequence=VSP\_003208, VSP\_003214;  
 Name=Mdm2-B;  
 IsoId=Q00987-4; Sequence=VSP\_003209;  
 Name=Mdm2-C;  
 IsoId=Q00987-5; Sequence=VSP\_003211;  
 Name=Mdm2-D;  
 IsoId=Q00987-6; Sequence=VSP\_003210;  
 Name=Mdm2-E;  
 IsoId=Q00987-7; Sequence=VSP\_003212, VSP\_003213;  
 Name=Mdm2-alpha;  
 IsoId=Q00987-8; Sequence=VSP\_003207;  
 TISSUE SPECIFICITY: Ubiquitous. Isoforms MDM2-A, -B, -C, -D and -E  
 are observed in a range of human cancers but absent in normal  
 tissues.  
 INDUCTION: By DNA damage.  
 DOMAIN: Region I is sufficient for binding p53 and inhibiting its  
 G1 arrest and apoptosis functions. It also binds p73 and E2F1.  
 Region II contains most of a central acidic region required for  
 interaction with ribosomal protein L5 and a putative C4-type zinc  
 finger. The RING finger domain which coordinates two molecules of  
 zinc interacts specifically with RNA whether or not zinc is  
 present and mediates the hetero-oligomerization with MDM4. It is  
 also essential for its ubiquitin ligase E3 activity toward p53 and  
 itself.  
 PTM: Phosphorylated in response to ionizing radiation in an ATM-  
 dependent manner.  
 DISEASE: Seems to be amplified in certain tumors (including soft  
 tissue sarcomas, osteosarcomas and gliomas). A higher frequency of  
 splice variants lacking p53 binding domain sequences was found in  
 late-stage and high-grade ovarian and bladder carcinomas. Four of  
 the splice variants show loss of p53 binding.  
 MISCELLANEOUS: MDM2 RING finger mutations that failed to  
 Query Match 98.9%; Score 548; DB 1;  
 Best Local Similarity 99.1%; Pred. No. 2.4e-50;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 SQIPASQETLVPRPKPLKLKSAGKQDTYTMKEVLFYQYIMTRKLVIDEQKQIVH 60  
 17 SQIPASEQETLVPRPKPLKLKSAGKQDTYTMKEVLYQYIMTRKLVIDEQKQIVH 76

61 CSNDLIGDLPFGVPSFSYKEHRKITYMTYRNLYVNNQESSDSGTSVSEN 109  
 77 CSNDLIGDLPFGVPSFSYKEHRKITYMTYRNLYVNNQESSDSGTSVSEN 125

RESULT 5  
 MDM2 CANFA  
 ID\_MDM2\_CANFA STANDARD;  
 AC P56751; Q93KN5;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein  
DE Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (cdm2).  
GN Name=MDM2;  
OS Canis familiaris (Dog).  
OC Vertebrata; Craniata; Chordata; Metazoa; Animalia;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1] RP SEQUENCE OF 1-484 FROM N.A.  
RX MEDLINE=20218866; PubMed=10754200; DOI=10.1016/S0304-3835(99)00427-9;  
RN Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,  
RA Argyle D.J.;  
RT "Cloning, sequence analysis and expression of the cDNAs encoding the canine and equine homologues of the mouse double minute 2 (mdm2) proto-oncogene.";  
RT Cancer Lett. 152:9-13 (2000).  
RN [2] RP SEQUENCE FROM N.A. (ISOFORMS MDM2 AND MDM2-ALPHA).  
RX MEDLINE=20065171; PubMed=10597303; DOI=10.1038/sj.onc.1203182;  
RA Veldhoven N., Mercalde S., Milner J.,  
RT "A novel exon within the mdm2 gene modulates translation initiation in vitro and disrupts the p53-binding domain of mdm2 protein.";  
RL Oncogene 18:7026-7033 (1999).  
CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and apoptosis by binding its transcriptional activation domain.  
CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2, toward p53 and itself. Permits the nuclear export of p53 and targets it for proteasome-mediated proteolysis (By similarity).  
CC -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By similarity).  
CC -!- SUBUNIT: Binds p53, p73, ARF (P14), ribosomal protein L5 and specifically to RNA. Can interact also with retinoblastoma protein (RB), E1A-associated protein E2F30 and the E2F1 transcription factor (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed predominantly in the nucleoplasm (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=2;  
Name=Mdm2;  
Tboid=P55950-1; Sequence=Displayed;  
Name=Mdm2-alpha;  
CC Tboid=P5650-2; Sequence=VSP 003206;  
CC -!- TISSUE SPECIFICITY: Isoform Mdm2-alpha is present in lymphoid and testicular tissues.  
CC -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its G1 arrest and apoptosis functions. It also binds p73 and E2F1. Region II contains most of a central acidic region required for interaction with ribosomal protein L5 and a putative C4-type zinc finger. The RING finger domain which coordinates two molecules of zinc interacts specifically with RNA whether or not zinc is present and mediates the hetero-oligomerization with Mdm4. It is also essential for its ubiquitin ligase E3 activity toward p53 and itsself (By similarity).  
CC -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.  
CC -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.  
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.  
CC -!- SIMILARITY: Contains 1 SWIB domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL; AF322416; AA67833\_1; -;  
DR HSSP; Q9UW78; IYCR.  
CC DR InterPro; IPR010984; MDM2.  
CC DR InterPro; IPR003121; SWIB.  
CC DR InterPro; IPR001876; Znf\_RanGDP.  
CC DR InterPro; IPR001841; Znf\_ring.

CC DR SMART; SM00184; zf-RanBP1; 1.  
CC DR PROSITE; PS01338; ZF\_RING\_2; 1.  
CC DR PROSITE; PS50199; ZF\_RING\_2; 1.  
CC DR PROSITE; PS00188; ZF\_RING\_1; FALSE\_NEG.

DR Pfam; PF02201; SWIB; 1.  
DR Pfam; PF00641; zf-RanBP; 1.  
DR SMART; SM00184; zf-RanBP2\_1; 1.  
DR PROSITE; PS01558; ZF\_RANBP2\_1; 1.  
DR PROSITE; PS50199; ZF\_RANBP2\_2; 1.  
DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.

DR PROSITE; PS50089; ZF\_RING\_2; 1.  
KW Alternative splicing; Ligase; Metal-binding; Nuclear protein; Ub1 conjugation pathway; Zinc; Zirc-finger.

DR KW Ubl conjugation pathway; Zinc; Zinc-finger.

FT DOMAIN 227 107  
FT DOMAIN 179 185  
FT DOMAIN 190 202  
FT DOMAIN 210 304  
FT DOMAIN 215 215  
FT DOMAIN 242 331  
FT DOMAIN 243 301  
FT DOMAIN 299 328  
FT ZN\_FINGER 434 475  
FT ZN\_FINGER 462 469  
FT VARSPLIC 1 61  
FT VARSPLIC 11 11  
FT VARSPLIC 238 239  
FT VARSPLIC 487 AA; 54696 MW; 600DB470A32AE69 CRC64;  
SQ SEQUENCE 77 CSNDLIGDLFGVPSFSVKEHRKITYTMIRNLVNNQESSDSGTSVSEN 109  
SQ SEQUENCE 77 CSNDLIGDLFGVPSFSVKEHRKITYTMIRNLVNNQEPSDGTSVSEN 125

Query Match 96.8%; Score 536; DB 1; Length 487;  
Best Local Similarity 96.3%; Pred. No. 4.7e-49;  
Matches 105; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SQIPSEQETLVRPKLKLKSKGAQDTTYMKBEVLFLYGOXTMTKRLYDEKQOHIVH 60  
Db 17 SQIPSEQETLVRPKLKLKSKGAQDTTYMKBEVLFLYGOXTMTKRLYDEKQOHIVY 76

Qy 61 CSNDLIGDLFGVPSFSVKEHRKITYTMIRNLVNNQESSDSGTSVSEN 109  
Db 77 CSNDLIGDLFGVPSFSVKEHRKITYTMIRNLVNNQEPSDGTSVSEN 125

RESULT 6  
Q9GMZ6 ID Q9GMZ6 PRELIMINARY; PRT; 487 AA.  
AC 09GMZ6; DT 01-MAR-2001 (TREMBUREL 16, Created)  
DT 01-JUN-2003 (TREMBUREL 16, Last sequence update)  
DT DE MDM2.  
GN Name=mdm2;  
Canis familiaris (Dog).  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buttharia; Carnivora; Fissipedia; Canidae; Canis.  
OC NCBI\_TaxID=9615;  
OX RN [1];  
RN SEQUENCE FROM N.A.  
RP TISSUE=Liver;  
RC Setoguchi A., Tsujimoto H.; EMBL/GenBank/DDJB database.  
RA RL Submitted (AUG-1999) to the EMBL/GenBank/DDJB database.  
DR EMBL; AB031276; BAB1975\_1; -.  
DR HSSP; Q9UW78; IYCR.  
DR GO; GO:0005730; C:nucleolus; ISS.  
CC GO; GO:0005654; C:nucleoplasm; ISS.  
CC GO; GO:0017163; F:negative regulator of basal transcription a...; ISS.  
CC GO; GO:0005515; F:protein binding; ISS.  
DR InterPro; IPR010984; MDM2.  
DR InterPro; IPR003121; SWIB MDM2.  
DR InterPro; IPR001876; Znf\_RanGDP.  
DR InterPro; IPR001841; Znf\_ring.

DR Pfam; PF02201; SWIB; 1.  
DR SMART; SM00184; zf-RanBP; 1.  
DR PROSITE; PS01338; ZF\_RING\_2; 1.  
DR PROSITE; PS50199; ZF\_RANBP2\_2; 1.

DR	PROSITE; PS50089; ZF RING 2;	ZF RING 2;	Score 536 ; DB 2;	Length 487;		
SQ	SEQUENCE 487 AA; 54724 MW; 34FC5C6A18D7744 CRC64;					
	Best Local Similarity 96.3%; Pred. No. 4.7e-49;					
	Matches 105; Conservative 2; Mismatches 2;	Indels 0;	Gaps 0;			
Qy	1 SQIPASQETLVRPKPLLKLLKKSVERAQKDVTMKEVLFYQYIMTRKLYDEKOQHIVH 60					
Db	17 SQIPASQETLVRPKPLLKLLKKSVERAQKDVTMKEVLFYQYIMTRKLYDEKOQHIVH 76					
Qy	61 CSNDLIGDLFGYPSPFSYKEHRKITYMITYRNLYVNVQESSSDSGTSEEN 109					
Db	77 CSNDLIGDLFGYPSPFSYKEHRKITYMITYRNLYVNVQHEPDSGTSSEN 125					
<b>RESULT 7</b>						
ID	MDM2_HORSE	HORSE	STANDARD;	PRT;	491 AA.	
AC	P56951;					
DT	30-MAY-2000 (Rel. 39, Created)					
DT	30-MAY-2000 (Rel. 39, Last sequence update)					
DT	05-JUL-2004 (Rel. 44, Last annotation update)					
DE	Ubiquitin-protein ligase E3 Mdm2 (BC_6.3.2.-) (p53-binding protein Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Edm2).					
GN	Name=MDM2;					
OS	Equus caballus (Horse).					
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC					
OX	NCBI_TaxID=9796;					
RN	[1]					
RP	SEQUENCE FROM N.A. MEDLINE=20218866; PubMed=10754200; DOI=10.1016/S0304-3835(99)00427-9;					
RA	Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H., Argyle D.J.; RT "Cloning, sequence analysis and expression of the cDNAs encoding the proto-oncogene," RT canine and equine homologues of the mouse double minute 2 (mdm2) Cancer Lett. 152:9-13 (2000).					
CC	-!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By similarity).					
CC	-!- SUBUNIT: Binds p53, p73, ARF (P14), ribosomal protein L5 and specifically to RNA. Can interact also with retinoblastoma protein (RB), E1A-associated protein EP300 and the E2F1 transcription factor (By similarity).					
CC	-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed predominantly in the nucleoplasm (By similarity).					
CC	-!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its G1 arrest and apoptosis functions. It also binds p73 and E2F1. Region II contains most of a central acidic region required for interaction with ribosomal protein L5 and a putative C4-type zinc finger. The RING finger domain which coordinates two molecules of zinc interacts specifically with RNA whether or not zinc is present and mediates the hetero-oligomerization with MDM4. It is also essential for its ubiquitin ligase E3 activity toward p53 and itself (By similarity).					
CC	-!- SIMILARITY: Belongs to the MDM2 / MDM4 family.					
CC	-!- SIMILARITY: Contains 1 RING-type zinc finger.					
CC	-!- SIMILARITY: Contains 1 SWIB domain.					
CC	SEQUENCE FROM N.A. RA					
CC	Q7YRZ8					
CC	PROTEIN: Q7YRZ8; PRELIMINARY;					
CC	AC					
CC	DT 01-OCT-2003 (TREMBLrel. 25, Created)					
CC	DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)					
CC	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)					
CC	DE Double minute 2 protein MDM2.					
GN	Name=mdm2;					
RN	[1]					
RP	SEQUENCE FROM N.A. RA					
CC	Q7YRZ8; RLM Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.					
CC	DR EMBL; AB09709; BAC78209.1; -					
CC	DR GO; GO:0005730; C:nucleolus; ISS.					
CC	DR GO; GO:0005654; C:nucleoplasm; ISS.					
CC	DR GO; GO:0017163; P:negative regulator of basal transcription a...; ISS.					
CC	DR GO; GO:000515; F:protein binding; ISS.					
CC	DR InterPro; IPRO010984; MDM2.					
CC	DR InterPro; IPRO03121; SWIB MDM2.					
CC	DR InterPro; IPRO01876; Zinc_RangDP.					
CC	DR InterPro; IPRO01841; Zinc_Ring.					
CC	DR Pfam; PF02201; SWIB; 1.					
CC	DR SMART; SM00184; ZF_RanBP; 1.					
CC	DR PROSITE; PS01358; ZF_RANBP2_1; 1.					

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DR	PROSITE; PS50199; ZF-RANBP2_2; 1.							
DR	PROSITE; PS50089; ZF-RING_2_1.							
SQ	SEQUENCE 491 AA; 55433 MW; D93E25D638E8B934 CRC64;							
	Query Match 96.2%; Score 533; DB 2; Length 491;							
	Best Local Similarity 95.4%; Pred. No. 1e-48;							
	Matches 104; Conservative 3; Mismatches 2; Indels 0; Gaps 0;							
Qy	1 SQIPASQETLVRPKPLKLKLSVGAQKDVTMKEVLFLYQYIMTRLYDEKQHIVH 60							
Db	17 SQMPASQETLVRPKPLKLKLSVGAQKDVTMKEVLFLYQYIMTRLYDEKQHIVY 76							
Qy	61 CSNDLIGDLFGVPSFSVYKEHRKLYTMIYRLVNVNQESSSDSGTS 109							
Db	77 CSNDLIGDLFGVPSFSVYKEHRKLYTMIYRLVNVNQESSSDSGTS 125							
	RESULT 9							
Q8WYJ2	ID Q8WYJ2; PRELIMINARY; PRT; 436 AA.							
ID	Q8WYJ2;							
AC	Q8WYJ2;							
DT	01-MAR-2002 (T=EMBLrel. 20, Created)							
DT	01-MAR-2002 (T=EMBLrel. 20, Last sequence update)							
DT	01-JUN-2003 (T=EMBLrel. 24, Last annotation update)							
DE	MDM2 protein.							
GN	Name=MDM2;							
OS	Homo sapiens (Human).							
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
OX	NCBI_TaxID:9606;							
RN	SEQUENCE FROM N.A. MEDLINE=21248713; PubMed=11351297;							
RX	Tamborini E., Delia Torre G., Lavarino C., Azzarelli A.,							
RA	Carpinelli P., Pierotti M.A., Pilotti S.,							
RA	"Analysis of the molecular species generated by MDM2 gene amplification in liposarcomas.";							
RT	RT							
RT	Int. J. Cancer 92: 790-796 (2001).							
RL	EMBL; AF092844; AAL40179.1.; -.							
DR	HSSP; Q90RMB8; LYCR.							
DR	GO; GO:0005730; C:nucleolus; ISS.							
DR	GO; GO:005654; C:nucleoplasm; ISS.							
DR	GO; GO:0017163; F:negative regulator of basal transcription a. . . ; ISS.							
DR	GO; GO:0005515; F:protein binding; ISS.							
DR	GO; GO:0000122; P:negative regulation of transcription from P. . . ; ISS.							
DR	Pfam; PF02201; SWIB; 1.							
DR	SMART; SM00184; RING_1.							
DR	DR: GO:0005730; C:nucleolus; ISS.							
DR	DR: GO:005654; C:nucleoplasm; ISS.							
DR	DR: GO:0017163; F:negative regulator of basal transcription a. . . ; ISS.							
DR	DR: GO:0005515; F:protein binding; ISS.							
DR	DR: GO:0000122; P:negative regulation of transcription from P. . . ; ISS.							
DR	Pfam; PF00041; zf-RanBP; 1.							
DR	SMART; SM00184; RING_1.							
DR	DR: GO:0005730; C:nucleolus; ISS.							
DR	DR: GO:005654; C:nucleoplasm; ISS.							
DR	DR: GO:0017163; F:negative regulator of basal transcription a. . . ; ISS.							
DR	DR: GO:0005515; F:protein binding; ISS.							
DR	DR: GO:0000122; P:negative regulation of transcription from P. . . ; ISS.							
SQ	SEQUENCE 436 AA; 49248 MW; 3C8F5E98BC4203A CRC64;							
	Query Match 89.9%; Score 498; DB 2; Length 436;							
	Best Local Similarity 93.3%; Pred. No. 5.2e-45;							
	Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;							
Qy	1 SQIPASQETLVRPKPLKLKLSVGAQKDVTMKEVLFLYQYIMTRLYDEKQHIVH 60							
Db	17 SQMPASQETLVRPKPLKLKLSVGAQKDVTMKEVLFLYQYIMTRLYDEKQHIVY 76							
Qy	61 CSNDLIGDLFGVPSFSVYKEHRKLYTMIYRLVNVNQESSSDSGTS 105							
Db	77 CSNDLIGDLFGVPSFSVYKEHRKLYTMIYRLVNVNQESSSDSGTS 121							
	RESULT 10							
MDM2_MOUSE	ID MDM2_MOUSE_STANDARD; AC P23804; Q61040; Q64330;							
	DT 01-NOV-1991 (Rel. 20, Created)							
	DT 15-JUL-1998 (Rel. 36, Last sequence update)							
	DT 05-JUL-2004 (Rel. 44, Last annotation update)							

Note=Isoform Mdm2-D76 can also be produced by alternative initiation at Met-50 of isoform Mdm2-p90, but is produced more efficiently by alternative splicing;

Name=Rdm2-D76;

Isoid=P23804-2; Sequence=vSP\_003215;

Note=Does not bind to P53;

Event=Alternative initiation;

Comment=2 isoforms, Mdm2-p90 (shown here) and Mdm2-p76, are produced by alternative initiation at Met-1 and Met-50. Isoform Mdm2-p76 is produced more efficiently by alternative splicing; at low-level throughout embryo development and in adult tissues. Mdm2-p90 is much more abundant than Mdm2-p76 in testis, brain, heart, and kidney, but in the thymus, spleen, and intestine, the levels of the MDM2 proteins are roughly equivalent.

-!- INDUCTION: BY UV light.

-!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its G1 arrest and apoptosis functions. It also binds p73 and B2F1. Region II contains most of a central acidic region required for interaction with ribosomal protein L5 and a putative C4-type zinc finger. The RING finger domain which coordinates two molecules of zinc interacts specifically with RNA whether or not zinc is present and mediates the hetero-oligomerization with MDM4. It is also essential for its ubiquitin ligase E3 activity toward p53 and itself.

-!- PTM: Phosphorylated in response to ionizing radiation in an ATM-dependent manner.

CC -!- DISEASE: The gene for this protein is amplified in a mouse tumor cell line.

CC -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.

CC -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.

CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

CC -!- SIMILARITY: Contains 1 SWIB domain.

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DR EMBL; U40145; CRA1634.; -;

DR EMBL; U47944; AAB91167.1; -;

DR EMBL; U47945; AAB90930.1; JOINED.

DR EMBL; U47916; AAB90930.1; JOINED.

DR EMBL; U47937; AAB90930.1; JOINED.

DR EMBL; U47938; AAB90930.1; JOINED.

DR EMBL; U47939; AAB90930.1; JOINED.

DR EMBL; U47940; AAB90930.1; JOINED.

DR EMBL; U47941; AAB90930.1; JOINED.

DR EMBL; U47942; AAB90930.1; JOINED.

DR EMBL; U47943; AAB90930.1; JOINED.

DR EMBL; U47944; AAB90930.1; -.

PIR; S15349; S15349.

HSSP; Q9UWTB; 1YCR.

DR MGd; MGd: 96352; Mdm2.

DR GO; GO:0005634; C:nucleus; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.

DR GO; GO:0030163; P:protein catabolism; IDA.

DR GO; GO:0015567; P:protein ubiquitination; IDA.

DR GO; GO:0007089; P:traversing start control point of mitotic c...; IDA.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR001876; Znf\_RanGDP.

DR Pfam; PF02201; SWIB.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS01358; ZP\_RANBP2-1; 1.

DR PROSITE; PS50199; ZP\_RANBP2-2; 1.

DR PROSITE; PS00518; ZP\_RING\_1; FALSE\_NEG.

DR PROSITE; PS50089; ZP\_RING\_2; 1.

KW Alternative initiation; Alternative splicing; Ligase; Metal-binding;

KW Nuclear protein; Phosphorylation; Proto-oncogene;

KW Ub1 conjugation pathway; Zinc; Zinc-finger.

FT CHAIN 1 489

FT CHAIN 50 489

FT INIT MET 50 50

FT DOMAIN 27 107

FT DOMAIN 176 182

FT DOMAIN 183 195

FT DOMAIN 203 213

FT DOMAIN 208 302

FT DOMAIN 240 329

FT DOMAIN 221 299

FT ZN\_FING 297 326

FT ZN\_FING 436 477

FT DOMAIN 464 471

FT VARSPLIC 1 49

FT CONFLICT 203 203

FT CONFLICT 419 419

FT CONFLICT 486 486

SQ SEQUENCE 489 AA; 54543 MW; 4ABF499B9203BDP4 CRC64;

Query Match 88.2% Score 488.5; DB 1; Length 489;

Best Local Similarity 87.2%; Pred. No. 6.2e-44;

Matches 95; Conservative 8; Mismatches 3; Indels 3; Gaps 1;

Qy 1 SQIPASQEQTLYVRPKPLKLKIKSQAQDTTYTMKVEFLVIGQYMTKRLYDEKQHIVH 60

Db 17 SQIPASQEQTLYVRPKPLKLKIKSQAQDTTYTMKVEFLVIGQYMTKRLYDEKQHIVY 76

Qy 61 CSNDLIGDGFVGPSPFSEVKERKITYMIYRNLYVNVQESSDSGTYSSEN 1.09

Db 77 CSNDLIGDGFVGPSPFSEVKERKITYMIYRNLYVAVSQ--DSGTISSES 122

RESULT 11

Q91XK7 PRELIMINARY; PRT; 489 AA.

ID Q91XK7

AC Q91XK7;

DT 01-DBC-2001 (TREMBLrel. 19, Created)

DT 01-DBC-2001 (TREMBLrel. 19, Last sequence update)

DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)

DB Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:12000011P22 product transformed mouse T33 cell double minute 2, full insert sequence (Transformed mouse 3T3 cell double minute 2) (Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430022B10 product:transformed mouse 3T3 cell double minute 2, full insert sequence).

DE Name=Mdm2;

GN Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Murinae; Mus.

OC NCBI\_TaxID:10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J, and NOD; TISSUE=lung, and Thymus;

RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-5679(99)03004-9;

RX Carninci P.; Hayashizaki Y.; RT "High efficiency full-length cDNA cloning." ;

RX Meth. Enzymol. 303:19-44(1999). ;

RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J, and NOD; TISSUE=lung, and Thymus;

RX MEDLINE=2108566; PubMed=11217851; DOI=10.1038/35055500;

RX RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection." ;

RN Nature 409:685-690(2001). ;

[3] RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; and NOD; TISSUE=Lung, and Thymus;  
RA THE FANTOM Consortium  
RA THE RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs";  
RL Nature 420:563-573 (2002).  
RN

[4] RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;  
MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630 (2000).  
RN

[5] RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J, and NOD; TISSUE=Lung, and Thymus;  
MEDLINE=2050913; PubMed=11076851; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagacka S., Sasaki N., Carninci P.,  
Kondo H., Akiyama K., Nishi K., Kitsunai T., Itoh M.,  
Sumi N., Ishii Y., Nakamura S., Hazana M., Nishina T., Harada A.,  
Yamamoto R., Matsumoto H., Nishina T., Tashiro K., Hiraoka T.,  
Fujimura S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanuki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kiria A., Hayashizaki Y.;  
RT "TRIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 capillary sequencer.";  
RL Genome Res. 10:1757-1771 (2000).  
RN

[6] RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
Hanagata T., Hara A., Hayatsu N., Hiramoto K., Hirao T., Hori F.,  
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
Kawai J., Koijima Y., Kono H., Kouda M., Koya S., Kurihara C.,  
Matsuura T., Miyazaki R., Nishi K., Nomura K., Numazaki R., Ohno M.,  
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
Sano H., Sasaki D., Shibata K., Shiba T., Shinagawa A., Shiraki T.,  
Ra Suzuki Y., Suzukawa H., Tagami M., Tagawa A., Tanaka T.,  
Tejima Y., Toyta T., Yamagura T., Yasunishi A., Yoshida K., Yoshino M.,  
Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
RN

[7] RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Mouse;  
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klaushier D., Collins F.S., Wagner L., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,  
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soress M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Praha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalain D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzewinski M.I., Skalska U., Smailus D.E., Schenck J.B., Schein J.B.,  
Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN

[8] RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Mouse;

[9] RN Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.  
RN SEQUENCE FROM N.A.  
RC TRAIN-NOD; TISSUE=Thymus;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
Hayashida K., Hayatsu N., Hiramoto K., Hirao T., Hiraoka T.,  
Hori F., Imotani K., Ishii Y., Itoh M., Kaga Y., Kajiwara T.,  
Kato H., Kawai J., Kojima Y., Kondo S., Konoh H., Kouda M., Koya S.,  
Kato H., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
Nishi K., Nomura K., Numazaki R., Ohno M., Ohnishi N.,  
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
Tagawa A., Takahashi F., Takagawa A., Shiraki T., Tomaru A.,  
Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AK004719; BAB23502.1;  
DR EMBL; BC050902; AAH0902.1;  
DR HSSP; Q9UW78; LYCR.  
DR MGD; MGI:96952; Mdm2.  
DR GO; GO:005730; C:nucleolus; IDA.  
DR GO; GO:000515; C:protein binding; IPI.  
DR GO; GO:0004842; Ubiquitin-protein ligase activity; IDA.  
DR GO; GO:0030163; P:protein catalysis; IDA.  
DR GO; GO:0016567; P:protein ubiquitination; IDA.  
DR GO; GO:0007089; P:traversing start control point of mitotic c. . . ; IDA.  
DR SMART; SM00184; RING; 1.  
DR Pfam; PF02201; SWIB; 1.  
DR PROSITE; PS50139; zf-RanBP2\_1.  
DR PROSITE; PS50089; zf-RanBP2\_2.  
DR PROSITE; PS50089; zf-RING\_2\_1.  
SQ SEQUENCE 489 AA; 5457 MW; 4ABF489A8203DF4 CRC64;  
Query Match 88.2%; Score 488.5; DB 2; Length 489;  
Best Local Similarity 87.2%; Pred. No. 6.2e-44;  
Matches 95; Conservative 8; Mis-matches 3; Indels 3; Gaps 1;

Qy 1 SQIPASEQETLVRPKPLKLKLSGTAQDVTYTMKEVLFLVGQYIMTKRLYDEKQHIVH 60  
Db 17 SQIPASEQETLVRPKPLKLKLSGTAQDVTYTMKEVLFLVGQYIMTKRLYDEKQHIVY 76

Qy 61 CSNDLGLDLFVPPSVKEERKITYMIRNLVVVQQESSDSGTSESEN 109  
Db 77 CSNDLGLDLFVPPSVKEERKITYMIRNLVVVQQESSDSGTSESEN 122

[10] RN RESULT 12  
RC Q8WQI3 PRELIMINARY; PRT; 118 AA.  
RA ID Q8WQI3  
AC Q8WQI3  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBrel. 20, Last sequence update)  
DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)  
DE MDM2 Protein (Fragment)  
DE NCBI\_TaxID=9606;  
GN Homo sapiens (Human)  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Buteraria; Primates; Catarrhini; Homino.  
OX NCBI\_TaxID=9606;  
RN SEQUENCE FROM N.A.  
RP MEDLINE=21248713; PubMed=11351297;  
RX Tamborini B., Della Torre G., Lavirino C., Azzarelli A.,  
RA Carpinelli P., Pierotti M.A., Piletti S.;  
RA "Analysis of the molecular species generated by MDM2 gene  
amplification in liposarcomas";  
RL Int. J. Cancer 92:790-796 (2001).  
DR AF032849; AAU40178.1; -.  
DR HSSP; Q9UMTB8; LYCR.  
DR GO; GO:0005634; C:nucleus; IEA.



DR PROSITE: PS50199; ZF\_RANBP2\_2; 1.  
 PT NON\_TER; 325 325 MW; B3C8509CCF5FD1ED CRC64;  
 SQ 325 AA;

Query Match 76.0%; Score 421; DB 2; Length 325;  
 Best Local Similarity 78.0%; Pred. No. 7.2e-37; Mismatches 8; Indels 0; Gaps 0;  
 Matches 78; Conservative 14; MisMatches 8; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLYRKPKLILKIKSVGAKDTYTMKEVLFYLQGYIMTKRLYDEKQOHIVH 60  
 Db 13 SPVSASEQEALVRPKPKLILKIKSVGAKDTYTMKEVLFYLQGYIMSKQLIDEKQOHIVH 72

Qy 61 CSNDLGLGFGVTSVKEHRKLYTMIYRNLYVNNQQESS 100  
 Db 73 CANDLGLGFGVTSVKEHRKLYSMSRNLAINQQST 112

## RESULT 15

QTE46 PRELIMINARY; PRT; 173 AA.  
 ID QTE46; AC QTE46; PR; 173 AA.  
 DR 01-JUN-2002 (TREMBLrel. 21; Last sequence update)  
 DR 01-JUN-2002 (TREMBLrel. 21; Last annotation update)  
 DR 01-JUN-2003 (TREMBLrel. 24; Last annotation update)  
 DE MDM2 isoform N1 40 protein.  
 GN Name=MDM2 isoform N1\_.  
 OS Homo sapiens (Human).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OM NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N A.  
 RC TISSUE: Kidney;  
 RA Bartel F., Pinkert D., Kappeler M., Baché M., Schmidt H., Taubert H.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AJ430614; CAD323252.1; -.  
 DR HSSP; Q9UMT8; IYCR.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.  
 DR GO; GO:000842; F:ubiquitin-protein ligase activity; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR InterPro; IPR010984; MDM2.  
 DR InterPro; IPR003121; SWIB MDM2.  
 DR InterPro; IPR001841; Znf\_Zing.  
 DR Pfam; PF02601; SWIB; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.

SQ SEQUENCE 173 AA; 19508 MW; AB26BECFA003B261 CRC64;

Query Match 72.6%; Score 402; DB 2; Length 173;

Best Local Similarity 80.4%; Pred. No. 3.9e-35; Mismatches 6; Indels 8; Gaps 1;

Matches 82; Conservative 6; MisMatches 6; Indels 8; Gaps 1;

Qy 1 SQIPASEQETLYRKPKLILKIKSVGAKDTYTMKEVLFYLQGYIMTKRLYDEKQOHIVH 60  
 Db 17 SQIPASEQETLYRKPKLILKIKSVGAKDTYTMKEVLFYLQGYIMTKRLYDEKQOHIVH 76

Qy 61 CSNDLGLGFGVTSVKEHRKLYTMIYRNLYVNNQQESS 102  
 Db 77 CSNDLGLGFGVTSVKEFRERETQ-----DKESVES 110

Search completed: February 16, 2005, 08:24:05  
 Job time : 172 secs